



# STIC Search Report

## Biotech-Chem Library

STIC Database Tracking Number: 105234

**TO: Phillip Gabel**

**Location: CM1/8B03&9E12**

**Art Unit: 1644**

**Wednesday, October 08, 2003**

**Case Serial Number: 09/730466**

**From: Toby Port**

**Location: Biotech-Chem Library**

**CM1-6A04**

**Phone: 308-3534**

**[toby.port@uspto.gov](mailto:toby.port@uspto.gov)**

### Search Notes

Dear Examiner Gabel,

Here are the results of your search.

Please feel free to contact me if you have any questions.

Toby Port

Result No.	Score	Query	Match	Length	DB	ID	Description	Summaries
1	475	100.0	112	23	ABB1992		Human transmembrane LFA-3 CD2 binding	FT
2	475	100.0	120	13	ARR27157		Human cell adhesion	FT
3	475	100.0	128	17	AW04361		Human cell adhesion	XX
4	475	100.0	133	17	AW04362		Human cell adhesion	PN
5	475	100.0	133	17	AW04363		Human LFA-3 antigen	XX
6	475	100.0	237	13	ARR20804		Human LFA-3 antigen	PD
7	475	100.0	237	17	ARR9142		Human LFA-3 antigen	XX
8	475	100.0	237	19	AW80441		Human LFA-3 antigen	PF
9	475	100.0	237	20	AW86189		Human LFA-3 antigen	XX

title: US-09-730-465-2_COPY_1_92	1 MVAGSDAGRALGVLSVYLL.....AFSSFKRNRYLDTYSGSLII 92	10 475 100.0 237 21 AAY96127
scoring table: BLASTM62		11 475 100.0 237 22 AAB02336
gapop 10.0 , Gapext 0.5		12 475 100.0 240 11 AAR05572
Maximum DB seq length: 0		13 475 100.0 240 11 AAR07604
Maximum DB seq length: 2000000000		14 475 100.0 240 13 AAR27162
Searched: 1107863 seqs, 15872653 residues		15 475 100.0 240 21 AY83134
total number of hits satisfying chosen parameters: 1107863		16 475 100.0 240 22 AAB61158
Minimum DB seq length: 0		17 475 100.0 240 22 AAB61158
Minimum DB seq length: 175.938 Million cell updates/sec		18 475 100.0 250 9 AAB81507
Post-processing: Maximum Match 0%		19 475 100.0 250 13 AAR27161
Post-processing: Maximum Match 100%		20 475 100.0 250 14 AAR34371
Listing first 45 summaries		21 475 100.0 250 15 AAR61271
Database : A_Geneseq_19Jun03.*		22 475 100.0 250 21 AY83136
1: /SIDS1/gcdata/geneseq/geneseqp-emb1/AA1980.DAT:*		23 475 100.0 250 22 AAB61160
2: /SIDS1/gcdata/geneseq/geneseqp-emb1/AA1981.DAT:*		24 475 100.0 250 22 AAB61157
3: /SIDS1/gcdata/geneseq/geneseqp-emb1/AA1982.DAT:*		25 475 100.0 250 23 AAB76225
4: /SIDS1/gcdata/geneseq/geneseqp-emb1/AA1983.DAT:*		26 475 100.0 256 24 AAO16017
5: /SIDS1/gcdata/geneseq/geneseqp-emb1/AA1984.DAT:*		27 475 100.0 256 24 ABP58178
6: /SIDS1/gcdata/geneseq/geneseqp-emb1/AA1985.DAT:*		28 475 100.0 347 13 AAR27163
7: /SIDS1/gcdata/geneseq/geneseqp-emb1/AA1986.DAT:*		29 475 100.0 347 12 AY83133
8: /SIDS1/gcdata/geneseq/geneseqp-emb1/AA1987.DAT:*		30 475 100.0 347 21 AY83133
9: /SIDS1/gcdata/geneseq/geneseqp-emb1/AA1988.DAT:*		31 475 100.0 347 23 ABB81994
10: /SIDS1/gcdata/geneseq/geneseqp-emb1/AA1989.DAT:*		32 475 100.0 347 23 AAB76228
11: /SIDS1/gcdata/geneseq/geneseqp-emb1/AA1990.DAT:*		33 475 100.0 347 24 AAO16017
12: /SIDS1/gcdata/geneseq/geneseqp-emb1/AA1991.DAT:*		34 475 100.0 351 23 ABB81995
13: /SIDS1/gcdata/geneseq/geneseqp-emb1/AA1992.DAT:*		35 472 99.4 240 14 AAR34222
14: /SIDS1/gcdata/geneseq/geneseqp-emb1/AA1993.DAT:*		36 472 99.4 240 14 AAR34272
15: /SIDS1/gcdata/geneseq/geneseqp-emb1/AA1994.DAT:*		37 472 99.4 250 14 AAR34221
16: /SIDS1/gcdata/geneseq/geneseqp-emb1/AA1995.DAT:*		38 469 98.7 237 18 AAW16687
17: /SIDS1/gcdata/geneseq/geneseqp-emb1/AA1996.DAT:*		39 464 97.7 237 18 AAW14182
18: /SIDS1/gcdata/geneseq/geneseqp-emb1/AA1997.DAT:*		40 463 97.5 237 18 AAW14182
19: /SIDS1/gcdata/geneseq/geneseqp-emb1/AA1998.DAT:*		41 459 96.6 250 13 ABBG18465
20: /SIDS1/gcdata/geneseq/geneseqp-emb1/AA1999.DAT:*		42 443 93.3 280 13 ABBG18495
21: /SIDS1/gcdata/geneseq/geneseqp-emb1/AA2000.DAT:*		43 328 69.1 71 13 AAR27158
22: /SIDS1/gcdata/geneseq/geneseqp-emb1/AA2001.DAT:*		44 328 69.1 134 13 ABBG18564
23: /SIDS1/gcdata/geneseq/geneseqp-emb1/AA2002.DAT:*		45 328 69.1 135 13 ABBG18564
24: /SIDS1/gcdata/geneseq/geneseqp-emb1/AA2003.DAT:*		

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULT 1	ABB1992	standard; Protein; 11.2 AA.
	ID	ABB1992
	XX	
	AC	ABB1992;
	XX	25-NOV-2002 (first entry)
	XX	Human transmembrane LFA-3 partial polypeptide.
	DE	
	DE	Human; immunosuppressive; antithyroid; dermatological; antiinflammatory; antipsoriatic; antirheumatic; antiarthritic; neuroprotective; vaccine; osteopathic; antidiabetic; gene therapy; CD2; LFA-3; interferon; IFN;
	KW	
	XX	
	OS	Homo sapiens.
	XX	
	FT	Location/Qualifiers
	FT	1..28
	FT	/note= "signal peptide"
	FT	29..84
	FT	/note= "partial mature protein fragment; the sequence after position 84 is not indicated in the complete sequence are not provided"

R	01-FEB-2001; 2001US-265964P.	XX	12-MAR-1992;	92EP-0104320.	
X	(BIOJ ) BIOGEN INC.	PF	XX		
X		PR	12-MAR-1991;	91US-0667971.	
I	Vaishnav AK, Cooper KD, Shrager D, McCormick TS;	PR	07-OCT-1991;	91US-0770967.	
X		XX			
R	WPI: 2002-65748B/70.	PA			
R	N PSDLB; A8Q79655.	PA			
X		PA			
X	Treating or preventing, by inhibiting CD2/LFA-3 interaction, an epidermal or dermal disorder, inflammatory and/or autoimmune disorder with aberrant T cell activity or proliferation -	PT			
IX		PT			
S	Disclosure: Page 58; 68bp; English.	PT			
X		PT			
X	The invention relates to treating or preventing an epidermal or dermal disorder, an inflammatory disorder and/or an autoimmune disorder with aberrant T cell activity. Proliferation. The method involves administering an inhibitor of the CD2/LFA-3 interaction, in combination with an auxiliary agent, thereby treating or preventing the epidermal or dermal disorder, the inflammatory disorder or the autoimmune disorder. The methods and compositions of the invention are useful for preventing or treating skin disorders characterized by increased T cell activation and abnormal antigen presentation in the dermis and epidermis, such as psoriasis, UV damage, atopic dermatitis, cutaneous T cell lymphoma, contact and atopic dermatitis, lichen planus, alopecia, vitiligo, urticaria. They may also be used in chronic inflammatory and autoimmune disorders such as diabetes mellitus, arthritis, rheumatoid arthritis, juvenile rheumatoid arthritis, spondarthrits, psoriatic arthritis, multiple sclerosis, encephalomyelitis, myasthenia gravis, systemic lupus erythematosis, autoimmune thyroiditis. The present sequence represents the human transmembrane LFA-3 partial amino acid sequence.	PT			
XX		PT			
SQ	Sequence 112 AA;	PT			
	Query Match Score 475; DB 23; Length 112;	PT			
	Best Local Similarity 100.0%; Pred. No. 4 5e-51;	PT			
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	PT				
QY	1 MVAGSDAGRAIGVLSSVCLLHCGRFISCSQQIYGYYGNTFHVPSNVPLKEVWKQK 60	QY	1 MVAGSDAGRAIGVLSSVCLLHCGRFISCSQQIYGYYGNTFHVPSNVPLKEVWKQK 60	QY	1 MVAGSDAGRAIGVLSSVCLLHCGRFISCSQQIYGYYGNTFHVPSNVPLKEVWKQK 60
Db	1 MVAGSDAGRAIGVLSSVCLLHCGRFISCSQQIYGYYGNTFHVPSNVPLKEVWKQK 60	Db	1 MVAGSDAGRAIGVLSSVCLLHCGRFISCSQQIYGYYGNTFHVPSNVPLKEVWKQK 60	Db	1 MVAGSDAGRAIGVLSSVCLLHCGRFISCSQQIYGYYGNTFHVPSNVPLKEVWKQK 60
QY	61 DKVAELENSEPRAFSEFKNRYLDTVSGSLTI 92	QY	61 DKVAELENSEPRAFSEFKNRYLDTVSGSLTI 92	QY	61 DKVAELENSEPRAFSEFKNRYLDTVSGSLTI 92
Db	61 DKVAELENSEPRAFSEFKNRYLDTVSGSLTI 92	Db	61 DKVAELENSEPRAFSEFKNRYLDTVSGSLTI 92	Db	61 DKVAELENSEPRAFSEFKNRYLDTVSGSLTI 92
	RESULT 2				
	AAR27157				
ID	AAR27157 standard; protein; 120 AA.	XX			
XX		XX			
AC	AAR27157;	AC			
XX		AAW04361;			
DT	27-JUN-1997 (first entry)	DT			
XX		XX			
DE	Human cell adhesion protein LFA-3.	DE			
XX		XX			
KW	Human; T cell; MOLT-4; cell adhesion; LFA-3; immunosuppression; cell line; immunosuppressant cell.	KW			
XX		KW			
OS	Homo sapiens.	OS			
XX		OS			
Synthetic.		PN			
XX		PN			
Key	Location/Qualifiers	XX			
FT region	2..78	XX			
FT	/note= "1..77 of these residues may be deleted"	XX			
FT region	89..120	PR			
FT	/note= "1..32 of these residues may be deleted"	PR			
XX		PR			
PN	EP503648-AL.	PR			
XX		XX			
PD	16-SEP-1992.	PA			
		PA			
		XX			

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

M protein - protein search, using sw model

run on: October 7, 2003, 11:13:47 ; Search time 40 Seconds  
(without alignments)  
221.188 Million cell updates/sec

title: US-09-730-465-2\_COPY\_1\_92

sequence: 1 MIVAGSDAGRAGLGVLYSVCIL..... AFSSEFKNRVYLDIVSGSLTI 92

scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR\_76-\*

1: Piri1:\*

2: Piri2:\*

3: Piri3:\*

4: Piri4:\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	475	100.0	250	2	A28564		lymphocyte function-associated antigen 3, transmembrane splice form precursor - human
2	742	14.7	244	2	A53244		lymphocyte function-associated antigen 3, transmembrane splice form precursor - human
3	70	14.7	546	2	T26568		hypothetical protein
4	69	14.6	389	2	T16326		hypothetical protein
5	67.5	14.2	240	2	JL0143		antigen BCML precursor protein
6	66	13.9	661	2	S49101		neuronal leucine-rich repeat protein
7	66	13.9	707	2	JC7763		neuronal leucine-rich repeat protein
8	65	13.7	416	2	T25036		hypothetical protein
9	65	13.7	1822	2	S44849		K12H4.8 protein -
10	64	13.5	243	2	T13504		NADH2 dehydrogenase
11	63.5	13.4	562	2	C82355		hypothetical protein
12	63	13.3	234	2	AD1649		weakly phage related
13	63	13.3	299	2	E90162		conserved hypothetical protein
14	63	13.3	608	2	S50912		probable membrane protein
15	62.5	13.2	274	2	S76154		hypothetical protein
16	62.5	13.2	635	2	T23874		NADH2 dehydrogenase
17	62.5	13.2	734	2	T13685		hypothetical protein
18	62	13.1	237	2	C70157		hypothetical protein
19	62	13.1	403	2	C33958		hypothetical protein
20	62	13.1	414	2	H84936		tRNA adenyllyltransferase
21	62	13.1	426	2	AB3933		probable malate dehydrogenase
22	62	13.1	426	2	C81733		malate oxidoreductase
23	62	13.1	510	2	ET70321		GMP synthase (glutamine synthetase)
24	61.5	12.9	522	2	EB8024		peptide methionine
25	61.5	12.9	522	2	GB1243		peptide methionine
26	61.5	12.9	741	2	T15711		NADH2 dehydrogenase
27	61.5	12.9	752	2	H9191		uncharacterized protein
28	61	12.9	836	2	E97851		hypothetical protein
29	61	12.8	344	2	T00993		probable beta-1,3-

RESULT 2

30	61	12.8	347	2	S41638		T-cell surface glycoprotein
31	61	12.8	405	2	S41917		ornithine-oxo-acid
32	61	12.8	424	1	XNBYO		dolichyl-diphosphoinositide-linked protein
33	61	12.8	508	1	A30007		myosin I heavy chain
34	61	12.8	539	2	T2041		signal peptidase-1
35	61	12.8	1107	1	S52517		alpha-1,2-galactosidase
36	60.5	12.7	275	2	E83655		probable acyl-coenzyme A acyltransferase
37	60.5	12.7	351	2	T4762		hypothetical protein
38	60.5	12.7	380	2	T17423		protoporphyrinogen
39	60.5	12.7	475	2	T33979		centaurin, retinol-binding protein
40	60.5	12.7	490	2	T38088		variant-specific sigma-1 receptor
41	60.5	12.7	1210	2	C59431		glycine receptor beta-1
42	60.5	12.7	2924	2	T18378		alpha-N-acetylgalactosaminidase
43	60	12.6	496	2	JH0165		gap junction protein beta-1
44	60	12.6	526	2	S46459		gap junction protein beta-2
45	60	12.6	526	2	JC7248		gap junction protein beta-3

#### ALIGNMENTS

RESULT 1	A28564	lymphocyte function-associated antigen 3, transmembrane splice form precursor - human
		Alternative names: CD58 antigen; surface glycoprotein IIA-3
	C; Species: Homo sapiens (man)	C; Comment: 15-Dec-1988 #sequence_change 15-Dec-1988 #text_change 02-Aug-2002
	C; Accession: A28564; S01369	R; Wallner, B.P.; Frey, A.Z.; Tizard, R.; Mattaliano, R.J.; Hession, C.; Sanders, M.E.; Exp. Med. 166, 923-932, 1987
	A; Title: Primary structure of lymphocyte function-associated antigen 3 (LFA-3). The A; Reference number: A28564; PMID:8809714	R; See: B.
	A; Molecule type: mRNA	Nature 329, 840-842, 1987
	A; Residues: 1-250 <WAL>	A; Title: An LFA-3 cDNA encodes a phospholipid-linked membrane protein homologous to A; Reference number: S01269; PMID:88039074; PMID:3313052
	A; Accession: S01269	A; Cross-references: EMBL:306236; NID:934349; PDB:CA29622.1; PID:934350
	A; Residues: 1-235; 'VI' <SRE>	C; Comment: For an alternative splice form, see PIR:SP1269.
	A; Cross-references: EMBL:306236; NID:934349; PDB:CA29622.1; PID:934350	C; Comment: For an alternative splice form, see PIR:SP1269.
	A; Cross-references: EMBL:306236; NID:934349; PDB:CA29622.1; PID:934350	C; Genetics:
	A; Gene: GDB:CD58; LFA3	A; Cross-references: PDB:120580; OMIM:153420
	A; MDP position: 1P13-1P13	C; Superfamily: human B-cell antigen gp19; immunoglobulin homology
	C; Keywords: alternative splicing; glycoprotein; phosphatidylinositol linkage; surface	F; 1:130/domain: signal sequence #status predicted <SIG>
	C; Comment: For an alternative splice form, see PIR:SP1269.	F; 31-250/Domain: lymphocyte function-associated antigen 3 transmembrane splice form
	C; Genetics:	F; 40-159/Domain: immunoglobulin homology <IMM>
	A; Cross-references: PDB:120580; OMIM:153420	F; 40,94-109,135,169,195/Binding site: carbohydrate (Asn) (covalent) #status predicted
	C; Superfamily: human B-cell antigen gp19; immunoglobulin homology	Query Match 100.0%; Score 475; DB 2; Length 250;
	F; 1:130/domain: signal sequence #status predicted <SIG>	Best Local Similarity 100.0%; Pred. No. 2.3e-45;
	F; 31-250/Domain: lymphocyte function-associated antigen 3 transmembrane splice form	Mismatches 0; Mismatches 0; Gaps 0; Gaps 0;
	F; 40-159/Domain: immunoglobulin homology <IMM>	Indels 0; Indels 0;
QY	1 MIVAGSDAGRAGLGVLYSVCILCFGTISCFSQIQYGVVGNVTPHYPNSVNPYLEVKLNKOK 60	Matches 92; Matches 92; Conservations 0; Conservations 0.
Db	1 MIVAGSDAGRAGLGVLYSVCILCFGTISCFSQIQYGVVGNVTPHYPNSVNPYLEVKLNKOK 60	
QY	61 DKAELENSEFRAFSSFKRNVYLDIVSGSLTI 92	
Db	61 DKAELENSEFRAFSSFKRNVYLDIVSGSLTI 92	

3244 leukocyte antigen CD48 precursor - human  
 Alternate names: B-cell surface glycoprotein Elast-1; CD48; leukocyte antigen Huly-M3;  
 Species: Homo sapiens (man)  
 Date: 19-May-1994 #sequence\_revision 19-May-1994 #text\_change 23-Jul-1999  
 Accession: A51244; A53245; A27236; A39689; A41320  
 Korinek, V.; Stefanova, I.; Angelissova, P.; Hilgert, I.; Horejsi, V.  
 Immunogenetics 33, 108-112, 1991  
 Title: The human leucocyte antigen CD48 (MEL-102) is closely related to the activation  
 Reference number: A53244; PMID:91153857; PMID:1993350  
 Accession: A53244  
 Molecule type: mRNA  
 Residues: 1-213 <OR>  
 Cross-references: GB:M37766; PID:9187518; PID:AAA36211\_1; PID:9187519  
 Note: part of this sequence, including the amino end of the mature protein, was determined  
 Vaughan, H.A.; Henning, M.M.; Purcell, D.F.J.; McKenzie, I.F.C.; Sandrin, M.S.  
 Immunogenetics 33, 113-117, 1991  
 Title: The isolation of cDNA clones for CD48.  
 Reference number: A53245; M01D:91153858; PMID:1993351  
 Molecule type: mRNA  
 Residues: 1, N-3-243 <VA>  
 Cross-references: GB:M9904; PID:9180138; PID:AAA62834\_1; PID:9180139  
 Staunton, D.E.; Morley-Lawson, D.A.  
 MBO J., 3695-3701, 1987  
 Title: Molecular cloning of the lymphocyte activation marker blast-1.  
 Reference number: A27236; MUID:8811558; PMID:2828034  
 Accession: A27236  
 Molecule type: mRNA  
 Residues: 1-65 /'N-67-243 <STA>  
 Cross-references: EMBL:X06341; PID:929454; PID:CAA29647\_1; PID:9732754  
 Note: the authors translated the codon AAT for residue 66 as Ile and ACG for residue 2  
 Fisher, R.C.; Thorley-Lawson, D.A.  
 Mol. Cell. Biol. 11, 1614-1623, 1991  
 Reference number: A39689; MUID:91141511; PMID:1847502  
 Molecule type: DNA  
 Residues: 1-27 <F1>  
 Cross-references: GB:M6911; PID:917949; PID:AAA35602\_1; PID:917945  
 R.Del Porto, P.; Mami-Chouaib, F.; Bruneau, J.M.; Jitsukawa, S.; Dumas, J.; Harnois, M.;  
 J. Exp. Med. 173, 1339-1344, 1991  
 Title: Characterization of the Epstein-Barr virus-inducible gene encoding the human le  
 Reference number: A39689; MUID:91141511; PMID:1847502  
 Accession: A3689  
 Molecule type: DNA  
 Residues: 1-27 <F1>  
 Cross-references: GB:M6911; PID:917949; PID:AAA35602\_1; PID:917945  
 R.Del Porto, P.; Mami-Chouaib, F.; Bruneau, J.M.; Jitsukawa, S.; Dumas, J.; Harnois, M.;  
 J. Exp. Med. 173, 1339-1344, 1991  
 Title: Characterization of the Epstein-Barr virus-inducible gene encoding the human le  
 Reference number: A39689; MUID:91141511; PMID:1847502  
 Accession: A51220  
 Molecule type: protein  
 A1:Residues: 'D', 30-39, 'R', 41-43, 'S', 45-53, 'A', 55-56; 63-74, 'E', 76-81, 'X', 83, 'X', 87  
 C:Genetics: GDB:CD48 - BCML  
 A:Gene: GDB:CD48 - BCML  
 A:Cross-references: GDB:119725; OMIM:109530  
 A:Map Position: B-cell surface glycoprotein blast-1  
 C:Keywords: glycoprotein; Phosphatidylinositol linkage; surface antigen  
 F:1-28/Domain: 104,162,189,206/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 Query Match 15.7% Score 74.5% DB 2; Length 243;  
 Best Local Similarity 38.7% Pred. No. 1;  
 Matches 24; Conservative 12; Mismatches 21; Indels 5; Gaps 4;  
 QY 36 VVYG-NYTFHVSNPV-LKRVLWKKQKD-KVAELENSEERAF SSFKNRNYLDTVSSKL 90  
 DB 35 VVGSNTVNLNISSELSLNPENYKQLTWFTEDQKIVWEDSRSKYFESKFKGRVRLDPOSGAL 94  
 QY 91 RI 92  
 DB 95 RI 96

RESULT 3  
 T26568 3  
 hypothetical protein Y26D4A.10 - Caenorhabditis elegans  
 C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
 C;Accession: T26558  
 R;White, S.  
 Submitted to the EMBL Data Library, September 1999  
 A;Reference number: 220234  
 A;Accession: T26568  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: DNA  
 A;Residues: 1-546 <WIL>  
 A;Cross-references: EMBL:AI110478; NID:61542139; PIDN:CA854346\_1; CESP:Y26D4A.10  
 A;Experimental source: clone Y26D4A  
 C;Genetics:  
 A;Gene: CESP:Y26D4A.10  
 A;Introns: 415/3; 506/3  
 Query Match 14.7% Score 70; DB 2; Length 546;  
 Best Local Similarity 28.9% Pred. No. 8 2;  
 Matches 22; Conservative 11; Mismatches 27; Indels 16; Gaps 3;  
 QY 19 LILHCGFISCFSQOYVGVY-----GNTFHVPSPNVLPIKEVWKKQ--KDKV-- 63  
 DB 163 LTHLFGFTECYNLLIGYGRKHNLSSYRSPEKNNSITSSNPONTFARMVINKLQWIPKILP 222  
 64. -AELENSEERAFSSFK 78  
 DB 1:1  
 223 CLENQKLNLNFSNK 238  
 RESULT 4  
 T16326 hypothetical protein F41C6\_7 - Caenorhabditis elegans  
 C;Species: Caenorhabditis elegans  
 C;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Sep-1999  
 C;Accession: T16326  
 R;Geissel, C.  
 Submitted to the EMBL Data Library, October 1995  
 A;Cross-references: EMBL:U39745; NID:91049470; PID:91049476; PIDN:AAA80448\_1; CESP:F41C6.  
 A;Description: The sequence of C. elegans cosmid F41C6.  
 A;Reference number: Z18495  
 A;Accession: T16326  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: DNA  
 A;Residues: 1-389 <GET>  
 A;Cross-references: EMBL:U39745; NID:91049470; PID:91049476; PIDN:AAA80448\_1; CESP:F41C6.  
 A;Gene: CESP:F41C6\_7  
 A;Introns: 50/3; 118/3; 136/3; 154/3; 189/3; 209/3; 235/2; 264/3; 300/3; 327/3; 362/2  
 Query Match 14.6% Score 69.5% DB 2; Length 389;  
 Best Local Similarity 28.3% Pred. No. 6 4;  
 Matches 17; Conservative 14; Mismatches 28; Indels 1; Gaps 1;  
 QY 14 LSVVCLLHCFCFESQOYVGVYGVNTFHVPSPNVLPIKEVWKKQVAYELNSEFRA 73  
 DB 289 IYAVCIAHSYKIISSNOSMFIVGVITYHV-GNRAIVEYCEVENQNRTEIQSKFSA 347  
 RESULT 5  
 JL0143 antigen BCML precursor - mouse  
 N;Alternative names: CD48 antigen homolog sgp-60; OK45 antigen, Blast-1 antigen  
 C;Species: Mus musculus (house mouse)  
 C;Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 31-Jan-2000  
 C;Accession: JL0143; S21319; A47469; B47469  
 R;Wong, Y.W.; Williams, A.F.; Kingsmore, S.F.; Seldin, M.F.  
 J. Exp. Med. 171, 2115-2130, 1990  
 A;Title: Structure, expression, and genetic linkage of the mouse BCML (OK45 or Blast-  
 region on mouse chromosome 3.  
 A;Reference number: JL0143; MUID:90278362; PMID:1693656  
 A;Molecule type: mRNA  
 A;Residues: 1-240 <WON>  
 A;Cross-references: EMBL:X17501; NID:950134; PIDN:CAA35542\_1; PID:950135  
 R;Wong, Y.W.; Williams, A.F.; Kingsmore, S.F.; Seldin, M.F.

A protein - protein search, using sw model													
Run on:	October 7, 2003, 11:12:57	Search time 22 Seconds											
Sequence:		1 MVGGSDAGRAGLYSVCLL..... AFSSFKRNVYLDIVSGSEI 92											
Scoring table:	BLOSUM62	Minimum DB seq length:	0	Maximum DB seq length:	200000000	post-processing:	Maximum Match 0% Listing First 45 summaries						
Database:	SwissProt_41:	Total number of hits satisfying chosen parameters: 127863 seqs, 47026705 residues											
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.													
SUMMARIES													
Result No.	Score	Query	Match	Length	DB	ID	Description						
1	475	100.0	250	1	LEA3_HUMAN	P19256	homo sapiens						
2	74.5	15.7	243	1	CD48_HUMAN	P03326	homo sapiens						
3	67.5	14.2	240	1	CD48_MOUSE	P18181	mus musculus						
4	63.5	13.4	611	1	CDMS_WIGR	P08330	w glicusom						
5	63	13.3	379	1	ASPN_HUMAN	Q9PxxJ	homo sapiens						
6	62	13.1	414	1	CC4_BUGAI	P17169	buchnera a						
7	62	13.1	461	1	PICC_RHOCA	P23462	rhodobacter						
8	62	13.1	510	1	GUTA_AQDAE	Q66601	aquifex ae						
9	62	13.1	552	1	YHUL_SCHPO	Q9clv8	schizosaccharomyces pombe						
10	61.5	12.9	522	1	MSAB_NEIMA	P14930	n peptide						
11	61.5	12.9	522	1	MSAB_NEIMA	Q91jw8	n peptide						
12	61.5	12.9	522	1	MSAB_NEIMA	Q91jn8	n peptide						
13	61.5	12.9	741	1	NC5C_CUCIN	Q32007	cichorium						
14	61	12.8	347	1	CT22_HORSE	P37998	equus caballus						
15	61	12.8	373	1	ASPN_MOUSE	Q90mg4	mus musculus						
16	61	12.8	408	1	METK_DROME	P40200	drosophila						
17	61	12.8	424	1	ORT_YEAST	P07991	saccharomyces cerevisiae						
18	61	12.8	508	1	GSBD_CHICK	P12244	gallus gallus						
19	61	12.8	1107	1	M11E_RAT	Q63356	rattus norvegicus						
20	60.5	12.7	193	1	Y331_STRPO	Q975x4	sulfolobus						
21	60.5	12.7	262	1	S17A_MOUSE	Q90409	streptococcus						
22	60.5	12.7	490	1	YHAN7_SCHPO	Q10662	schizosaccharomyces pombe						
23	60.5	12.7	1136	1	CD22_HUMAN	Q9P48	homo sapiens						
24	60	12.6	496	1	GRB_MOUSE	P48168	mus musculus						
25	60	12.6	496	1	GRB_RAT	P20781	rattus norvegicus						
26	60	12.6	526	1	S17A_MOUSE	Q9gr39	mus musculus						
27	59.5	12.5	609	1	RPA1_XENLA	Q01588	xenopus laevis						
28	59.5	12.5	741	1	NEF5C_ASTCO	P51097	steller corona						
29	59.5	12.5	974	1	AVXB_BEDDO	P12522	leishmania						
30	59.5	12.5	1056	1	ACUB_YEAST	Q12674	saccharomyces cerevisiae						
31	59	12.4	268	1	TIJIA_BOVIN	P08831	bos taurus						
32	59	12.4	288	1	CD80_HUMAN	Q35681	homo sapiens						
33	59	12.4	314	1	TOPH_HREIN	P44976	haemophilus						

RESULT 1						
LFA3_HUMAN						
ID	LFA3_HUMAN	STANDARD;	PRY;	250 AA.		
AC	P19256; 09619;					
DT	01-NOV-1990 (Rel. 16, Created)					
DT	01-NOV-1990 (Rel. 16, Last sequence update)					
DT	SEP-2003 (Rel. 42, Last annotation update)					
DE	Lymphocyte function-associated antigen 3 precursor (Ag3) (Antigen CD58) (Surface glycoprotein LFA-3).					
DE	CD58 OR LFA3.					
GN	OS					
OC	Hom sapiens (Human).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Homo.					
OX	NCBI_TaxID:9606;					
RN	SEQUENCE FROM N.A. (ISOFORM 1), AND PARTIAL SEQUENCE.					
RC	TISSUE=lymphocyte;					
RX	MEDLINE=88009714; Pubmed=3309127;					
RA	Wallner B.P., Frey A.Z., Tizard R., Mattaliano R.J., Hession C.,					
RA	Saunders M.E., Dustin M.L., Springer T.A.;					
RT	"Primary structure of lymphocyte function-associated antigen 3 (LFA-3). The ligand of the T lymphocyte CD2 glycoprotein."					
RL	J. Exp. Med. 166:923-932(1987).					
RN	SEQUENCE FROM N.A. (ISOFORM 2).					
RX	Medline=88039074; PubMed=3313052;					
RA	"LFA-3 cDNA encodes a phospholipid-linked membrane protein homologous to its receptor CD2."					
RT	Nature 329:840-842(1987).					
RN	[3]					
RX	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).					
RX	Medline=98199008; PubMed=9510189;					
RA	Wallich R., Bremer C., Brand Y., Roux M., Reister M., Meuer S.;					
RT	"Gene structure, promoter characterization, and basis for alternative mRNA splicing of the human CD58 gene."					
RL	J. Immunol. 160:2862-2871(1998).					
RN	[4]					
RX	X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 29-122.					
RX	Medline=99238273; PubMed=10200255;					
RA	Ikezumi S., Sparks L.M., van der Merwe P.A., Harlos K., Stuart D.I.,					
RA	Jones E.Y., Davis S.J.;					
RT	"Crystal structure of the CD2-binding domain of CD58 (lymphocyte function-associated antigen 3) at 1.8 $\AA$ : A resolution."					
RL	Proc. Natl. Acad. Sci. U.S.A. 96:2889-2894(1999).					
CC	-!- FUNCTION: LIGAND OF THE T LYMPHOCYTE CD2 GLYCOPROTEIN. THIS					
CC	INTERACTION IS IMPORTANT IN MEDIATING THYMOCYTE INTERACTIONS WITH					
CC	THYMIC EPITHELIAL CELLS, ANTIGEN-INDEPENDENT AND -DEPENDENT					
CC	INTERACTIONS OF T LYMPHOCYTES WITH TARGET CELLS AND ANTIGEN-PRESENTING CELLS, AND THE T LYMPHOCYTE ROSETTING WITH ERYTHROCYTES.					
CC	IN ADDITION, THE LFA-3/CD2 INTERACTION MAY PRIME RESPONSE BY BOTH					
CC	THE CD2+ AND LFA-3+ CELLS.					
CC	-!- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1) and					
CC	-!- attached to the membrane by a GPI-anchor (isoform 2).					
CC	-!- ALTERNATIVE PRODUCTS: Named isoforms=2;					
CC	-!- ALTERNATIVE splicing: Named isoforms=2;					

Name=Long;  
 IsoId=PI9256-1; SequenceDisplayed;  
 Name=Short;  
 IsoId=PI9256-2; Sequence=VSP\_002522; VSP\_002523;  
 -1- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.  
 -1- DATABASE: NAME=PROW; NOTE=CD guide CDB8 entry;  
 WWW="http://www.ncbi.nlm.nih.gov/procd/cd58.htm".

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DR EMBL; Y00656; CAA68668\_1; -;  
 DR EMBL; X06296; CAA2362\_1; -;  
 DR EMBL; Y14780; CAA75083\_1; -;  
 DR EMBL; Y14781; CAA75083\_1; JOINED;  
 DR EMBL; Y14782; CAA75083\_1; JOINED;  
 DR EMBL; Y14783; CAA75083\_1; JOINED;  
 DR EMBL; Y14784; CAA75083\_1; JOINED;  
 DR EMBL; Y14785; CAA75084\_1; JOINED;  
 DR EMBL; Y14786; CAA75084\_1; JOINED;  
 DR EMBL; Y14787; CAA75084\_1; JOINED;  
 DR EMBL; Y14788; CAA75084\_1; JOINED;  
 DR EMBL; Y14789; CAA75084\_1; JOINED;  
 DR EMBL; Y14790; CAA75084\_1; JOINED;  
 DR EMBL; Y14791; CAA75084\_1; JOINED;  
 DR EMBL; Y14792; CAA75084\_1; JOINED;  
 DR EMBL; Y14793; CAA75084\_1; JOINED;  
 DR EMBL; Y14794; CAA75084\_1; JOINED;  
 DR EMBL; Y14795; CAA75084\_1; JOINED;  
 DR EMBL; A28564; A28564;  
 DR PDB; 1CIZ; 05-APR-95;  
 DR PDB; 1CIZ; 22-JUN-98;  
 DR Genew; HGNC:1688; CD58.  
 DR MTM; 153420;  
 DR GO; GO:0005887; C:integral to plasma membrane; NAS.  
 DR GO; GO:0005115; F:protein binding activity; IPI.  
 DR GO; GO:0016337; P:cell -cell adhesion; NAS.  
 DR InterPro; IPR003599; Ig.  
 DR SMART; SM00409; Ig\_1.  
 DR PROSITE; PS00835; Ig-LIKE; FALSE NEG.  
 DR IMMUNOGLOBULIN domain; Glycoprotein; Transmembrane; Signal; GPI-anchor;  
 KW Alternative splicing; 3D-structure.

FT CHAIN 1 258 LYMPHOCYTE FUNCTION-ASSOCIATED ANTIGEN 3.  
 FT CHAIN 29 250 EXTRACELLULAR (POTENTIAL).  
 FT CHAIN 29 215 PROTEIN.  
 FT TRANSMEM 216 238 CYTOSOLIC (POTENTIAL).  
 FT DOMAIN 239 250 CYTOSLAMIC (POTENTIAL).  
 FT DOMAIN 135 194 IG-LIKE C2-TYPE.  
 FT DISULFID 142 187 BY SIMILARITY.  
 FT CARBOHYD 40 40 N-LINKED (GLONAC. . .).  
 FT CARBOHYD 94 94 N-LINKED (GLONAC. . .).  
 FT CARBOHYD 109 109 N-LINKED (GLONAC. . .).  
 FT CARBOHYD 135 135 N-LINKED (GLONAC. . .).  
 FT CARBOHYD 169 169 N-LINKED (GLONAC. . .).  
 FT CARBOHYD 195 195 N-LINKED (GLONAC. . .).  
 FT VARSPLIC 236 237 GI->VL (in isoform Short).  
 FT VARSPLIC 238 250 Missing (in isoform Short).  
 FT VSP\_002522. /FTID=VSP\_002523.  
 SEQUENCE 250 AA; 28147 MW; 34D635DF1D4FE2E C9c64;

Query Match 100.0%; Score 475; DB 1; Length 250;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-45;  
 Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MYAGSDAGRAGLVLSVYCLHCFGRISCFSSQTYGVYGVNTPHYPSPNVLKEVINKKKQK 60  
 1 MYAGSDAGRAGLVLSVYCLHCFGRISCFSSQTYGVYGVNTPHYPSPNVLKEVINKKKQK 60

61 DKAELENSEPRAFSEKNEYVLDTVSGSLTI 92  
 61 DKAELENSEPRAFSEKNEYVLDTVSGSLTI 92



DT 01-NOV-1996 (TREMBREL\_01, Last sequence update)  
 DT 01-MAR-2003 (TREMBREL\_23, Last annotation update)  
 DE LFA-3 (delta D2) Precursor.  
 OS Ovis sp.  
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Caprinae; Ovis.  
 NCBI\_TaxID=9939;  
 RN [1]  
 SEQUENCE FROM N.A.  
 RP RA Kakutani T.  
 RL Submitted (FEB-1994) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: D28583; BAA05919.1; -.  
 DR HSSP; P19256; 1CCZ.  
 DR InterPro: IPR003599; Ig.  
 DR SMART; SM00409; Ig; 1.  
 DR Signal.  
 KW FT SIGNAL 1 28 POTENTIAL.  
 SQ SEQUENCE 159 AA; 17645 MW; 592A37046CD983E CRC64;  
 Query Match 54.0%; Score 256.5; DB 6; Length 159;  
 Best Local Similarity 58.1%; Pred. No. 1.5e-21;  
 Matches 54; Conservative 9; Mismatches 29; Indels 1; Gaps 1;  
 QY 1 MVAASDAGALGVLSSVQVLLHGFISQSQIGVYGVNTFHVSNPVKEVNLKKK 60  
 DB 1 MAAGSAPGCAAGLGLVLFKLFDFISCVQDQYGMNGNTVYSESQPFTEIWKKGK 60  
 QY 61 DKVAEEL-ENSEFRAFSSEKRNRYLDTYSGLTI 92  
 DB 61 DKVYEWDTSGLRAFQSKRNRYLDTYSGLTI 93  
 RESULT 5  
 Q28754 PRELIMINARY; PRT; 227 AA.  
 ID ID Q28754 PRELIMINARY;  
 AC AC Q28754; PRELIMINARY;  
 DT DT 01-NOV-1996 (TREMBREL\_01, Created)  
 DT DT 01-NOV-1996 (TREMBREL\_01, Last sequence update)  
 DT DT 01-MAR-2003 (TREMBREL\_23, Last annotation update)  
 DE LFA-3 (delta TM) precursor.  
 OS Ovis sp.  
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Caprinae; Ovis.  
 NCBI\_TaxID=9939;  
 RN [1]  
 SEQUENCE FROM N.A.  
 RP RA Kakutani T.  
 RL Submitted (FEB-1994) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: D28585; BAA05921.1; -.  
 DR HSSP; P19256; 1CCZ.  
 DR InterPro: IPR003599; Ig.  
 DR SMART; SM00409; Ig; 1.  
 DR Signal.  
 KW FT SIGNAL 1 28 POTENTIAL.  
 SQ SEQUENCE 227 AA; 24760 MW; 1521A60B49E9B55 CRC64;  
 Query Match 54.0%; Score 256.5; DB 6; Length 227;  
 Best Local Similarity 58.1%; Pred. No. 2.3e-21;  
 Matches 54; Conservative 9; Mismatches 29; Indels 1; Gaps 1;  
 QY 1 MVAASDAGALGVLSSVQVLLHGFISQSQIGVYGVNTFHVSNPVKEVNLKKK 60  
 DB 1 MAAGSAPGCAAGLGLVLFKLFDFISCVQDQYGMNGNTVYSESQPFTEIWKKGK 60  
 QY 61 DKVAEEL-ENSEFRAFSSEKRNRYLDTYSGLTI 92  
 DB 61 DKVYEWDTSGLRAFQSKRNRYLDTYSGLTI 93  
 RESULT 4  
 Q28752 PRELIMINARY; PRT; 159 AA.  
 ID ID Q28752 PRELIMINARY; PRT; 159 AA.  
 AC AC Q28752; PRELIMINARY; PRT; 159 AA.  
 DT DT 01-NOV-1996 (TREMBREL\_01, Last sequence update)  
 DE LFA-3 (delta D2) Precursor.  
 OS Ovis sp.  
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Caprinae; Ovis.  
 NCBI\_TaxID=9939;  
 RN [1]  
 SEQUENCE FROM N.A.  
 RP RA Kakutani T.  
 RL Submitted (FEB-1994) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: D28586; BAA05922.1; -.  
 DR HSSP; P19256; 1CCZ.  
 DR InterPro: IPR003599; Ig.  
 DR SMART; SM00409; Ig; 1.  
 DR Signal.  
 KW FT SIGNAL 1 28 POTENTIAL.  
 SQ SEQUENCE 119 AA; 13732 MW; 4096AC6F45181505 CRC64;  
 Query Match 60.4%; Score 287; DB 4; Length 119;  
 Best Local Similarity 100.0%; Pred. No. 3.e-25;  
 Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 37 VIGNTYFHVPSNPVPLKEVNLKKQDKVVAELENSEFRASSFKRNRYLDTYSGLTI 92  
 DB 1 VIGNTYFHVPSNPVPLKEVNLKKQDKVVAELENSEFRASSFKRNRYLDTYSGLTI 56  
 RESULT 5  
 Q28753 PRELIMINARY; PRT; 159 AA.  
 ID ID Q28753 PRELIMINARY; PRT; 159 AA.  
 AC AC Q28753; PRELIMINARY; PRT; 159 AA.  
 DT DT 01-NOV-1996 (TREMBREL\_01, Last sequence update)  
 DE LFA-3 (delta TM) precursor.  
 OS Ovis sp.  
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Caprinae; Ovis.  
 NCBI\_TaxID=9939;  
 RN [1]  
 SEQUENCE FROM N.A.  
 RP RA Kakutani T.  
 RL Submitted (FEB-1994) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: D28587; BAA05923.1; -.  
 DR HSSP; P19256; 1CCZ.  
 DR InterPro: IPR003599; Ig.  
 DR SMART; SM00409; Ig; 1.  
 DR Signal.  
 KW FT SIGNAL 1 28 POTENTIAL.  
 SQ SEQUENCE 119 AA; 13732 MW; 4096AC6F45181505 CRC64;  
 Query Match 54.0%; Score 256.5; DB 6; Length 119;  
 Best Local Similarity 58.1%; Pred. No. 2.3e-21;  
 Matches 54; Conservative 9; Mismatches 29; Indels 1; Gaps 1;  
 QY 1 MVAASDAGALGVLSSVQVLLHGFISQSQIGVYGVNTFHVSNPVKEVNLKKK 60  
 DB 1 MAAGSAPGCAAGLGLVLFKLFDFISCVQDQYGMNGNTVYSESQPFTEIWKKGK 60  
 QY 61 DKVAEEL-ENSEFRAFSSEKRNRYLDTYSGLTI 92  
 DB 61 DKVYEWDTSGLRAFQSKRNRYLDTYSGLTI 93



MOLECULE TYPE: protein

JS-07-940-861-12

Query Match 100.0%; Score 475; DB 1; Length 240;  
Best Local Similarity 100.0%; Pred. No. 1..1e-51;  
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2Y 1 MVAGSDAGRALSIVYCLLHCQGFISCFSSQIYGVYGVNTFHVPSNVPLKEYLWKKK 60  
2b 1 MVAGSDAGRALSIVYCLLHCQGFISCFSSQIYGVYGVNTFHVPSNVPLKEYLWKKK 60

2Y 61 DKVAELENSEFRAFSSFKNRVYLDITVSGSLI 92  
61 DKVAELENSEFRAFSSFKNRVYLDITVSGSLI 92

RESULT 2  
US-08-459-512-12  
; Sequence 12, Application US/08459512  
; GENERAL INFORMATION:  
; APPLICANT: BIOPEN, INC.  
; APPLICANT: WALLNER, Barbara P.  
; APPLICANT: MILLER, Glenn T.  
; APPLICANT: ROSA, Margaret D.  
; TITLE OF INVENTION: CD2-BINDING DOMAIN OF LYMPHOCYTE  
; TITLE OF INVENTION: FUNCTION ASSOCIATED ANTIGEN 3  
; NUMBER OF SEQUENCES: 43  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Neave  
; STREET: 875 Third Avenue  
; CITY: New York  
; STATE: New York  
; ZIP: 10022-6250  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOSS/MS-DOS  
; SOFTWARE: Patent Release #1.0, version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/459,657  
; FILING DATE: 02-JUN-1995  
; CLASSIFICATION: 424  
; PRIORITY APPLICATION DATA:  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOSS/MS-DOS  
; SOFTWARE: Patent Release #1.0, version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/459,512  
; FILING DATE: 02-JUN-1995  
; CLASSIFICATION: 514  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US92/02050  
; FILING DATE: 12-MAR-1992  
; APPLICATION NUMBER: US 07/667,971  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: US 07/770,967  
; FILING DATE: 07-OCT-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: HALLEY, James F., Jr.  
; REGISTRATION NUMBER: B151CIP2  
; FILING DATE: 12-MAR-1991  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: US 07/667,971  
; FILING DATE: 07-OCT-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: HALLEY, James F., Jr.  
; REGISTRATION NUMBER: B151CIP2  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: US 07/770,967  
; FILING DATE: 07-OCT-1991  
; TELEFAX: (212)715-0600  
; TELEFAX: (212)715-0673  
; TELEFAX: 14-3367  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 240 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein

Query Match 100.0%; Score 475; DB 2; Length 240;  
Best Local Similarity 100.0%; Pred. No. 1..1e-51;  
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVAGSDAGRALSIVYCLLHCQGFISCFSSQIYGVYGVNTFHVPSNVPLKEYLWKKK 60  
Db 1 MVAGSDAGRALSIVYCLLHCQGFISCFSSQIYGVYGVNTFHVPSNVPLKEYLWKKK 60

QY 61 DKVAELENSEFRAFSSFKNRVYLDITVSGSLI 92  
Db 61 DKVAELENSEFRAFSSFKNRVYLDITVSGSLI 92

Query Match 100.0%; Score 475; DB 1; Length 240;  
Best Local Similarity 100.0%; Pred. No. 1..1e-51;  
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVAGSDAGRALSIVYCLLHCQGFISCFSSQIYGVYGVNTFHVPSNVPLKEYLWKKK 60  
Db 61 DKVAELENSEFRAFSSFKNRVYLDITVSGSLI 92

Result	No.	Score	Query	Match	Length	DB	ID	Description	Summaries
1	475	100.0	240	9	US-09-796-033-4	Sequence 4, Appli			
2	475	100.0	240	9	US-09-730-465-4	Sequence 4, Appli			
3	475	100.0	250	9	US-09-796-033-2	Sequence 2, Appli			
4	475	100.0	250	9	US-09-730-465-2	Sequence 2, Appli			
5	475	100.0	250	12	US-10-436-523-61	Sequence 61, Appli			
6	475	100.0	250	15	US-10-207-655-113	Sequence 113, Appli			
7	475	100.0	347	9	US-09-796-033-8	Sequence 8, Appli			
8	475	100.0	347	9	US-09-730-465-8	Sequence 8, Appli			
9	475	100.0	347	14	US-10-091-236-17	Sequence 17, Appli			
10	475	100.0	347	15	US-10-091-313-7	Sequence 7, Appli			
11	475	100.0	347	15	US-10-091-268-7	Sequence 7, Appli			
12	74.5	15.7	96	9	US-09-864-761-47502	Sequence 47502, Appli			
13	74.5	15.7	243	11	US-09-860-8368-13	Sequence 13, Appli			
14	74.5	15.7	243	12	US-10-436-523-62	Sequence 62, Appli			
15	74.5	15.7	243	15	US-10-207-655-111	Sequence 111, Appli			





3 01-FEB-2001; 2001US-265564P.  
4 (BIOJ ) BIOPEN INC.  
X Vaishnaw AK, Cooper KD, Shrager D, McCormick TS;  
X WPI: 2002-657488/70.  
R N-PSDB; AB079655.  
X X Treating or preventing, by inhibiting CD2/LFA-3 interaction, an epidermal or dermal disorder, inflammatory and/or autoimmune disorder with aberrant T cell activity or proliferation -  
X Disclosure: Page 58; 68pp; English.  
X X The invention relates to treating or preventing an epidermal or dermal disorder, an inflammatory disorder and/or an autoimmune disorder in a subject with aberrant T cell activity or proliferation. The method involves administering an inhibitor of the CD2/LFA-3 interaction, in combination with an auxiliary agent, thereby treating or preventing the epidermal or dermal disorder, the inflammatory disorder or the autoimmune disorder. The methods and compositions of the invention are useful for preventing or treating skin disorders characterized by increased T cell activation and abnormal antigen presentation in the dermis and epidermis, such as psoriasis, UV damage, atopic dermatitis, cutaneous T cell lymphoma, contact and atopic dermatitis, lichen planus, alopecia, vitiligo, urticaria. They may also be used in chronic inflammatory and autoimmune disorders such as diabetes mellitus, arthritis, rheumatoid arthritis, juvenile rheumatoid arthritis, osteoarthritis, psoriatic arthritis, multiple sclerosis, encephalomyelitis, myasthenia gravis, systemic lupus erythematosus, autoimmune thyroiditis. The present sequence represents the human transmembrane LFA-3 partial amino acid sequence.

XX Sequence 112 AA;

Query Match 100.0%; Score 327; DB 23; Length 112;  
Best Local Similarity 100.0%; Pred. No. 2.2e-34;  
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2Y 1 LHCGRFISCFSSQIYGVYGNVTHYPSNVPLKEYLWKKQDKVAELENSERAFSSFKN 60  
Db 20 LHCGRFISCFSSQIYGVYGNVTHYPSNVPLKEYLWKKQDKVAELENSERAFSSFKN 79  
61 R 61  
2Y 61 R 61  
Db 80 R 80

RESULT 2  
ID AAR2157  
XX AC AAR2157;  
XX DT 25-MAR-2003 (updated)  
XX DT 20-MAY-1998 (first entry)  
XX DE LFA-3 CD2 binding domain polypeptide #2.  
XX KW Lymphocyte associated antigen-3; T-lymphocyte accessory molecule.  
XX OS Synthetic.  
XX Key Location/Qualifiers  
FT region 2..78  
FT region /note= "1-77 of these residues may be deleted"  
FT region 89..120  
FT region /note= "1-32 of these residues may be deleted"

RESULT 3  
ID AAW04361  
XX AC AAW04361;  
XX DT 27-JUN-1997 (first entry)  
XX DE Human cell adhesion protein LFA-3.  
XX KW Human; T cell; M03T-4; cell adhesion; LFA-3; immunosuppression;  
XX KW cell line; immunosuppressant cell.  
XX OS Homo sapiens.  
XX PN WO9633217-A1.  
XX PD 24-OCT-1996.  
XX PP 15-APR-1996;  
XX PP 15-APR-1996;  
XX PR 27-DEC-1995;  
XX PR 19-APR-1995;  
XX PR 04-JUL-1995;  
XX PA (KANP ) KANEKA FUCHI KAGAKU KOGYO KK.  
XX

XX PE 12-MAR-1992; 92EP-0104320.  
XX PR 12-MAR-1991; 91US-0667971.  
XX PR 07-OCT-1991; 91US-0770967.  
XX PA (BIOJ ) BIOPEN INC.  
XX PI Miller GR, Rosa MD, Wallner BP;  
XX DR WPI: 1992-309760/38.  
XX PT CD2-binding domain of lymphocyte function associated antigen-3 and DNA - for diagnosing and treating inflammation and autoimmune diseases, e.g. systemic lupus erythematosus and rheumatoid arthritis.  
XX PS Claim 1; Page 52-53; 85pp; English.  
XX PS Claim 1; Page 52-53; 85pp; English.  
XX CC This polypeptide can bind to CD2. The N-terminal Met is opt. absent. The N-terminal and C-terminal portions can be deleted.  
CC The polypeptide and its functional deletion mutants may be used to treat acute and chronic inflammation, autoimmune disease and for immunomodulation. The polypeptides can also form the N-terminal part of a fusion protein. The polypeptides and fusion proteins may also be used to inhibit T-cell activation and the proliferation of peripheral blood lymphocytes. Multimeric proteins can be formed from the polypeptides and/or fusion proteins. The multimers have enhanced affinity for CD2. See also AAR2157-9.  
CC (Updated on 25-MAR-2003 to correct PN field.)  
XX Sequence 120 AA;  
Query Match 100.0%; Score 327; DB 13; Length 120;  
Best Local Similarity 100.0%; Pred. No. 2.4e-34;  
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LHCGRFISCFSSQIYGVYGNVTHYPSNVPLKEYLWKKQDKVAELENSERAFSSFKN 60  
Db 20 LHCGRFISCFSSQIYGVYGNVTHYPSNVPLKEYLWKKQDKVAELENSERAFSSFKN 79  
61 R 61  
Db 80 R 80

GenCore version 5.1.6					
Copyright (c) 1993 - 2003 Compugen Ltd.					
protein - protein search, using sw model					
Search on:	October 7, 2003, 16:45:48	Search time:	7.47549	Seconds	
		(without alignments)			
		784.736	Million cell	updates/sec	
title:	US-09-730-465-2_COPY_20_80				
perfect score:	327				
sequence:	1 LHCFFGTSCFSQQIYGVYV.....DKVAEIDENSEPRAFSSEKFRN 61				
scoring table:	BLOSUM62				
GapOp:	10.0	Gapext:	0.5		
number of hits searched:	283308	seqs:	96168682	residues	
total number of hits satisfying chosen parameters:	283308				
DB seq length:	0				
maximum DB seq length:	200000000				
list processing:	Minimum Match 0%				
	Maximum Match 100%				
	Listing first 45 summaries				
database :	PIR_76;*				
	1: PIR2;*				
	2: PIR3;*				
	3: PIR4;*				
	4: PIR5;*				
Pre. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.					
SUMMARIES					
%					
Query	Score	Match	Length	DB	ID
Result No.	Score	Match	Length	DB	ID
1	327	100.0	250	2	A28564
2	67	20.5	546	2	T26568
3	63.5	19.4	562	2	CB2355
4	62	19.0	416	2	T25036
5	60.5	18.5	275	2	BS83655
6	60.5	18.5	508	1	A10007
7	60.5	18.5	1822	2	S44849
8	60.5	18.5	2924	2	T18378
9	60	18.3	405	2	S41917
10	60	18.3	619	2	C56714
11	60	18.3	852	2	AD0050
12	59.5	18.2	273	2	BE4608
13	59	18.0	294	2	AD1649
14	59	18.0	344	2	T0093
15	59	18.0	475	2	T12955
16	59	18.0	511	2	BE13332
17	58.5	17.9	508	2	F71865
18	58.5	17.9	666	2	S34197
19	58	17.7	237	2	C70157
20	58	17.7	299	2	EP0162
21	58	17.7	679	2	SS4299
22	58	17.7	719	2	DD0083
23	58	17.7	737	2	T13504
24	57.5	17.6	401	2	BS6501
25	57.5	17.6	425	2	T24111
26	57.5	17.6	632	2	CB1261
27	57.5	17.6	786	2	AG6375
28	57	17.6	1157	2	WD-40 repeat-protein
29	57	17.4	509	2	F22L4_11 protein



Scoring table:	BLOSUM62	Gapop 10.0 , Gapext 0.5	
Searched:	127863 seqs, 47026705 residues		
Total number of hits satisfying chosen parameters:	127863		
Minimum DB seq length: 0			
Maximum DB seq length: 2000000000			
Post-processing: Maximum Match 0%			
Post-processing: Listing first 45 summaries			
Database :	SwissProt_41:*		
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.			
SUMMARIES			
Result No.	Score	Query Match Length DB ID	Description
1	327	100.0 250 1 LFA3_HUMAN	P19256 homo sapien
2	61.5 18.8 379 1 ASPN_HUMAN	Q9bxn1 homo sapien	
3	60.5 18.5 373 1 ASPN_MOUSE	Q99mc4 mus musculus	
4	60.5 18.5 508 1 GSPB_CHICK	P12244 gallus gallus	
5	60 18.3 408 1 METK_DRONE	P40320 drosophila	
6	59 18.0 438 1 ARLY_CLOSE	P59616 clostridium	
7	59 18.0 511 1 GUA1_CAME	Q9pn49 campylobacter	
8	58.5 17.9 508 1 GUA1_HELPJ	Q9zkq4 halobacteria	
9	58 17.6 679 1 YTK1A_CRALP	Q42675 craterostig	
10	57.5 17.6 552 1 YH11L_SFHO	Q9c0v8 schizosaccharomyces	
11	56.5 17.3 299 1 RDGC_NEIGO	Q87408 neisseria	
12	56.5 17.3 299 1 RDGC_NEIGO	Q9jy02 neisseria	
13	56.5 17.3 299 1 RDGC_NEIGO	Q9jy2 neisseria	
14	56.5 17.3 974 1 ATXB_LEIDO	P12522 leishmania	
15	56.5 17.3 1656 1 ATCB_YEAST	Q12674 saccharomyces	
16	56 17.1 745 1 YJ00_YEAST	P47101 saccharomyces	
17	56 17.1 1107 1 MY1E_RAT	Q63356 ratmus norvegicus	
18	55 17.1 1363 1 ILPR_BRATIA	Q02466 brachioslobo	
19	55.5 17.0 348 1 Y25B_HELPJ	P56136 helicobacte	
20	55.5 17.0 350 1 Y25B_HELPJ	Q9zmh8 helicobacter	
21	55.5 17.0 974 1 CC15_YEAST	P27636 saccharomyces	
22	55 16.8 1656 1 Y942_MEITA	Q58352 methanococcus	
23	55 16.8 844 1 MC1EL_VARV	P33057 variola virus	
24	55 16.8 950 1 ORP1_HUMAN	Q9bxw6 homo sapien	
25	54.5 16.7 195 1 MOBA_YERPE	Q8zjs4 yersinia	
26	54.5 16.7 544 1 MLHL_HORYO	Q49873 hordeum vulgare	
27	54.5 16.7 898 1 TOP1_SYN3	P73810 synchocystis	
28	54.5 16.7 974 1 ATXA_LEIDO	P11718 leishmania	
29	54 16.5 833 1 PTIA_ECOLI	P32670 escherichia	
30	54 16.5 1010 1 CON1_CHICK	P14781 gallus gallus	
31	54 16.5 1109 1 MY1E_HUMAN	Q12965 homo sapien	
32	53.5 16.4 216 1 RL13_MOUSE	P47963 mus musculus	
33	53.5 16.4 304 1 PAGO_SALTY	Q30464 salmonella	

## ALIGNMENTS

RESULT 1		
LFA3_HUMAN	STANDARD;	PRT: 250 AA.
ID LFA3_HUMAN 5FK19;		
AC P19256; Q9GK19;		
DT 01-NOV-1990 (Rel. 16, Created)		
DT 01-NOV-1990 (Rel. 16, Last sequence update)		
DT 15-SEP-2003 (Rel. 42, Last annotation update)		
DE Lymphocyte function-associated antigen 3 precursor (Ag3) (Antigen)		
DE CD58 (Surface glycoprotein LFA-3).		
GN CD58 OR LFA3.		
OS Homo sapiens (Human).		
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
CA NCBI_TaxID:9606;		
RN	SEQUENCE FROM N.A. (ISOFORM 1), AND PARTIAL SEQUENCE.	
RC TISSUE-Erythrocyte;		
RX MEDLINE-88009714; PubMed=3309127;		
RA Wallner B.P., Frey A.Z., Tizard R., Mattaliano R.J., Hession C., Sanders M.E., Dustin M.L., Springer T.A.;		
RA "Primary structure of lymphocyte function-associated antigen 3 (LFA-3). The ligand of the T lymphocyte CD2 glycoprotein.",		
RT 3). The ligand of the T lymphocyte CD2 glycoprotein.",		
RT [1] Wallach R., Brenner C., Brand Y., Roux M., Reister M., Meuer S.;		
RL [2] J. Exp. Med. 166:923-932(1987).		
RN		
RP SEQUENCE FROM N.A. (ISOFORM 2);		
RX MEDLINE-88039074; PubMed=3313052;		
RA Seed B.;		
RA "An LFA-3 cDNA encodes a phospholipid-linked membrane protein homologous to its receptor CD2.",		
RT [3] Nature 329:840-842(1987).		
RL		
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).		
RX MEDLINE-98159008; PubMed=5510189;		
RA Wallach R., Brenner C., Brand Y., Roux M., Reister M., Meuer S.;		
RA "Gene structure, promoter characterization, and basis for alternative mRNA splicing of the human CD58 gene.",		
RT [4] J. Immunol. 160:2862-2871(1998).		
RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 29-122.		
RX MEDLINE-9218273; PubMed=1020255;		
RA Ikemizu S., Sparks L.M., van der Werf P.A., Harlos K., Stuart D.I., Jones E.Y., Davis S.J.;		
RA "Crystal structure of the CD2-binding domain of CD58 (lymphocyte function-associated antigen 3) at 1.8-A resolution.",		
RT [5] Proc. Natl. Acad. Sci. U.S.A. 96:4289-4294(1999).		
RL		
CC -!- FUNCTION: LIGAND OF THE T LYMPHOCYTE CD2 GLYCOPROTEIN. THIS INTERACTION IS IMPORTANT IN MEDIATING THYMOCYTE INTERACTIONS WITH THYMIC EPITHELIAL CELLS, ANTIGEN-INDEPENDENT AND -DEPENDENT INTERACTIONS OF T LYMPHOCYTES WITH TARGET CELLS AND ANTIGEN-PRESENTING CELLS, AND THE T LYMPHOCYTE ROSETTING WITH ERYTHROCYTES. IN ADDITION, THE LFA-3/CD2 INTERACTION MAY PRIME RESPONSE BY BOTH THE CD2+ AND LFA-3+ CELLS.		
CC -!- SUBCELLULAR LOCATION: TYPE I membrane protein (Isoform 1) and attached to the membrane by a GPI-anchor (Isoform 2).		
CC -!- ALTERNATIVE PRODUCTS: Named isoforms=2;		
CC -!- Event=Alternative splicing;		



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M protein - protein search, using sw model

run on: October 7, 2003, 16:45:18 ; Search time 18.0907 Seconds

(without alignments)  
870.128 Million cell updates/sec

effect score: 327 US-09-730-465-2\_COPY\_20\_80

coring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

Database : SPTRMBL\_23:\*

1: sp\_archaea:\*

2: sp\_bacteria:\*

3: sp\_fungi:\*

4: sp\_human:\*

5: sp\_invertebrate:\*

6: sp\_mammal:\*

7: sp\_mhc:\*

8: sp\_organelle:\*

9: sp\_phage:\*

10: sp\_plant:\*

11: sp\_rabbit:\*

12: sp\_virus:\*

13: sp\_vertebrate:\*

14: sp\_unclassified:\*

15: sp\_rvirus:\*

16: sp\_bacteriaph:\*

17: sp\_archeap:\*

RESULTS 1

Q9BRW0 ID Q9BRW0 PRELIMINARY;

AC Q9BRW0; DT 01-JUN-2001 (TREMBLrel. 17, Created)

DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE Similar to CD58 antigen, (Lymphocyte function-associated antigen 3).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Butheria; Primates; Catarrhini; Homino.

OX NCBI\_TaxID:9606; RN 11] SEQUENCE FROM N.A.

RP TISSUE=Brain; RC

RA Strausberg R.; DR Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.

RL DR EMBL; BC005930; AAH05930.1; -.

DR HSSP; P19256; ICCZ.

DR InterPro; IPR003599; IG.

DR SMART; SM00409; IG; 1.

SQ SEQUENCE 240 AA; 27044 MW; 431E44FFEDDF80B2 CRC64;

Query %

Result No. Score Match Length DB ID Description

Result No.	Score	Query	Match	Length	DB	ID	Description
1	327	100.0	240	4	Q9BRW0	Q9BRW0 homo sapien	Q14748 homo sapien
2	271	82.9	134	4	Q14748	Q14748 homo sapien	Q16193 homo sapien
3	230	70.3	119	4	Q16193	Q16193 homo sapien	Q28752 orvis sp. lf
4	165.5	50.6	159	6	Q28752	Q28752 orvis sp. lf	Q28754 orvis sp. lf
5	165.5	50.6	227	6	Q28754	Q28754 orvis sp. lf	Q28753 orvis sp. lf
6	165.5	50.6	253	6	Q28753	Q28753 orvis sp. lf	Q8396 sus scrofa
7	111.5	34.1	244	6	Q8396	Q8396 sus scrofa	Q9015 anas platyrhynchos
8	99	30.3	357	13	Q9015	Q9015 anas platyrhynchos	Q8934 uncultured
9	67	20.5	546	5	Q9015	Q9015 anas platyrhynchos	Q9krg2 vibrio cholerae
10	65	19.9	108	2	Q8934	Q8934 uncultured	Q8is6 oryza sativa
11	63.5	19.4	562	16	Q9krg2	Q9krg2 vibrio cholerae	Q8is9 plasmodium
12	63	19.3	515	10	Q8is7	Q8is7 oryza sativa	Q15795 plasmodium
13	62.5	19.1	413	5	Q8is33	Q8is33 plasmodium	Q8ic03 plasmodium
14	62.5	19.1	749	5	Q8is9	Q8is9 plasmodium	Q14748
15	62	19.0	205	5	Q8is7	Q8is7 oryza sativa	RESULT 2
16	62	19.0	252	5	Q8ic03	Q8ic03 plasmodium	Q14748

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

SEQUENCE FROM N.A.  
TISSUE=Brain;  
RA Strausberg R.; DR Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC005930; AAH05930.1; -.  
DR HSSP; P19256; ICCZ.  
DR InterPro; IPR003599; IG.  
DR SMART; SM00409; IG; 1.  
SQ SEQUENCE 240 AA; 27044 MW; 431E44FFEDDF80B2 CRC64;  
Query %

Query Match Length DB ID Description

Query Match Length DB ID Description

Query Match Length DB ID Description

D	Q14748	PRELIMINARY;	PRT;	134 AA.	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
C	Q14748;				OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
T	01-NOV-1996	(TREMBLrel. 01, Created)			NCBI_TaxID=939;	
T	01-NOV-1996	(TREMBLrel. 01, Last sequence update)			[1]	
T	01-DEC-2001	(TREMBLrel. 19, Last annotation update)				
RP	LFA-3 (delta D2)					
S	Homo sapiens (Human).					
C	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
C	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
X	NCBI_TaxID=9606;					
N	[1]					
P	SEQUENCE FROM N.A.					
P	Kakutani T.					
A	Submitted (FEB-1994) to the EMBL/GenBank/DBJ databases.					
L	EMBL; D2856; BAA05922.1; -.					
R	HSSP; P19255; 1CCZ.					
R	InterPro; IPR003599; Ig.					
R	SMART; SM00409; Ig; 1.					
T	NON_TER 1					
T	SEQUENCE 134 AA;					
Y	10 FSGQIYGVYGVNTFHVPSNVPLKEVLWKKDKVVAELENSEFRASSFKNR 61				RESULT 5	
b	1 FSQCIQYGVYGVNTFHVPSNVPLKEVLWKKDKVVAELENSEFRASSFKNR 52				ID Q28754	PRELIMINARY;
					AC Q28754;	ERT;
					AC Q28754;	227 AA.
RESULT 3					AC	
[D]	Q16393	PRELIMINARY;	PRT;	119 AA.	DT 01-NOV-1996	(TREMBLrel. 01, Created)
[C]	Q16393;				DT 01-NOV-1996	(TREMBLrel. 01, Last sequence update)
[T]	01-NOV-1996	(TREMBLrel. 01, Created)			DT 01-MAR-2003	(TREMBLrel. 23, Last annotation update)
[T]	01-NOV-1996	(TREMBLrel. 01, Last sequence update)			DE LFA-3 (delta TM) precursor.	
RP	LFA-3 (Fragment).				OS Ovis SP.	
[E]	Homo sapiens (Human).				OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
[S]	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;	
XX	NCBI_TaxID=9606;				NCBI_TaxID=939;	
XX	[1]				RN [1]	
RP	SEQUENCE FROM N.A.				RP SEQUENCE FROM N.A.	
[S]	MEDLINE:95398636; PubMed=7545392;				RA Kakutani T.	
XX	Kidby A.C., Hill V., Olsen I., Porter S.R.;				RL Submitted (FEB-1994) to the EMBL/GenBank/DBJ databases.	
RT	LFA-3 delta D2: a novel <i>in vivo</i> isoform of lymphocyte function-associated antigen 3 ";				DR D28585; BAA05921.1; -.	
RT	Biotech. Biochem. Biophys. Res. Commun. 214:200-205(1995).				DR HSSP; P19256; 1CCZ.	
DR	EMBL; S'9616; AAB0000.2; -.				DR InterPro; IPR003599; Ig.	
DR	HSSP; P19256; 1CCZ.				DR SMART; SM00409; Ig; 1.	
NON_TER	1				KW Signal.	
NON_TER	119				FT SIGNAL	1 28
FT	119 AA;				FT CHAIN	29 227 LFA-3 (DELTA TM).
SEQUENCE	13732 MW;				SQ SEQUENCE	227 AA; 24760 MW; 1521A800B49E9B55 CRC64;
QY	18 VIGNVTFHVPSNVPLKEVLWKKDKVVAELENSEFRASSFKNR 61				Query Match	50.6%; Score 165.5; DB 6; Length 227;
Db	1 VIGNVTFHVPSNVPLKEVLWKKDKVVAELENSEFRASSFKNR 44				Best Local Similarity 57.9%; Pred. No. 3.2e-12;	
					Matches 33; Conservative 6; Mismatches 17; Indels 1; Gaps 1;	
RESULT 4					Query Match	50.6%; Score 165.5; DB 6; Length 227;
ID	Q28752	PRELIMINARY;	PRT;	159 AA.	Best Local Similarity 57.9%; Pred. No. 3.2e-12;	
AC	Q28752;				Matches 33; Conservative 6; Mismatches 17; Indels 1; Gaps 1;	
DT	01-NOV-1996	(TREMBLrel. 01, Created)			Query Match	50.6%; Score 165.5; DB 6; Length 227;
DT	01-NOV-1996	(TREMBLrel. 01, Last sequence update)			Best Local Similarity 57.9%; Pred. No. 3.2e-12;	
DT	01-MAR-2003	(TREMBLrel. 23, Last annotation update)			Matches 33; Conservative 6; Mismatches 17; Indels 1; Gaps 1;	
DE	LFA-3 (delta D2) precursor.				Query Match	50.6%; Score 165.5; DB 6; Length 227;
OS	Ovis SP.				Best Local Similarity 57.9%; Pred. No. 3.2e-12;	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				Matches 33; Conservative 6; Mismatches 17; Indels 1; Gaps 1;	
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;				Query Match	50.6%; Score 165.5; DB 6; Length 227;
OC	Bovidae; Caprinae; Ovis.				Best Local Similarity 57.9%; Pred. No. 3.2e-12;	
NCBI_TaxID=939;	[1]				Matches 33; Conservative 6; Mismatches 17; Indels 1; Gaps 1;	



Q8756	Q8756	PRELIMINARY;	PRT;	515 AA.
AC	Q8756;			
DR	01-JUN-2002 (TREMBLrel. 21, Created)			
DT	01-OCT-2002 (TREMBLrel. 22, Last sequence update)			
DE	Cytochrome P450-like protein.			
GN	Oriza sativa (japonica cultivar-group)			
OC	Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Euphorbiidae; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Orzyeae; Orzyza.			
OX	Orzyza sativa L.			
RA	Salzberg S.E., Utterback T.R., Fieldblyum T.V., Kalb E., Quackenbush J., White O., Fraser C.M.;			
RA	VanAken S.E., Blunt S., Pai G., Tsitrkin T., Rigs F., Hsiao J., Zissmann V., Blunt S., Utterback T.R., Fieldblyum T.V., Kalb E., Quackenbush J., White O., Fraser C.M.;			
RA	Yuan Q., Ouyang S., Liu J., Moffat K.S., Hill J.N., Gansberger K., Bremer M., Burgess S., Hance M., Sivartsbey M., Buell C.R., Buell C.R., Hsiao J., Zissmann V., Blunt S., Pai G., Tsitrkin T., Rigs F., Hsiao J., Zissmann V., Blunt S., Utterback T.R., Fieldblyum T.V., Kalb E., Quackenbush J., White O., Fraser C.M.;			
RA	Orzya sativa chromosome 10 BAC OSJNB6005J14 genomic sequence.;"			
RA	Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.			
RA	-1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.			
RA	Interpro: IPR001128; P450_1.			
RA	PFam: PF0067; P450_1.			
RA	AC074232; AAM12483_1; -.			
RA	Gramene: QSTS6;			
RA	Interpro: IPR001128; Cytochrome_P450.			
RA	Heme; Monooxygenase; Oxidoreductase.			
RA	515 AA; 58129 MW; B83467EE81E0E85D CRC64;			
RA	SEQUENCE			
RA	5			
RA	5 GFSFCFSQIYGVYGNVTFHVPSPNVLKEYPLKEVWPKQDKVAELNESEFRAFSSR 58			
RA	61 GIVTC----YGMIGNTEDRTPS--MYEYIWIK----ENREAKVVSSE 98			
RA	61 GIVTC----YGMIGNTEDRTPS--MYEYIWIK----ENREAKVVSSE 98			
RA	Q8756	PRELIMINARY;	PRT;	562 AA.
RA	Q8756;			
RA	01-OCT-2000 (TREMBLrel. 15, Created)			
RA	01-OCT-2000 (TREMBLrel. 15, Last sequence update)			
RA	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
RA	DE Hypothetical Protein VC0184.			
RA	GN VC0184.			
RA	OS Vibrio cholerae.			
RA	OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibionales; Vibrionaceae; Vibrio.			
RA	OC NCBI_TAXID=666;			
RA	OX NCBI_TAXID=666;			
RA	RN [1]			
RA	RP SEQUENCE FROM N.A.			
RA	RC STRAIN=EL TOR NIE961 / Serotype: O1;			
RA	RC MEDLINE=204106833; PubMed=10952301;			
RA	RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L., Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Mayamensingh L.A., Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D., Erau Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P., McPoirier L., Utterback T., Fleischmann R.D., White O., Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C., Fraser C.M.			
RA	RT A sequence of both chromosomes of the cholera pathogen Vibrio cholerae.;"			
RA	RT DR AF004108; AAF93360_1; -.			
RA	RT DR TIGR; VC0184; -.			
RA	RT DR Hypothetical protein; Complete Proteome.			
RA	RA SEQUENCE 562 AA; 64954 MW; B7A93F4810C89523 CRC64;			
RA	RA Query Match 19.4%; Score 63.5%; DB 16; Length 562;			
RA	RA Best Local Similarity 27.8%; Pred. No. 27; Gaps 2;			
RA	RA Matches 15; Conservative 9; Mismatches 13; Indels 17; Gaps 2;			
RA	RA Q8756	PRELIMINARY;	PRT;	515 AA.
RA	RA AC Q8756;			
RA	RA DT 01-JUN-2002 (TREMBLrel. 21, Created)			
RA	RA DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)			
RA	RA DE Cytochrome P450-like protein.			
RA	RA GN OSB005J14.			
RA	RA OC			
RA	RA OC			
RA	RA OC			
RA	RA OX			
RA	RA Q8756	PRELIMINARY;	PRT;	515 AA.
RA	RA AC Q8756;			
RA	RA DT 01-JUN-2002 (TREMBLrel. 21, Created)			
RA	RA DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)			
RA	RA DE Cytochrome P450-like protein.			
RA	RA GN OSB005J14.			
RA	RA OC			
RA	RA OC			
RA	RA OX			
RA	RA Q8756	PRELIMINARY;	PRT;	515 AA.
RA	RA AC Q8756;			
RA	RA DT 01-JUN-2002 (TREMBLrel. 21, Created)			
RA	RA DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)			
RA	RA DE Cytochrome P450-like protein.			
RA	RA GN OSB005J14.			
RA	RA OC			
RA	RA OC			
RA	RA OX			

Q8756	Q8756	PRELIMINARY;	PRT;	515 AA.
AC	Q8756;			
DR	01-JUN-2002 (TREMBLrel. 21, Created)			
DT	01-OCT-2002 (TREMBLrel. 22, Last sequence update)			
DE	Cytochrome P450-like protein.			
GN	Oriza sativa (japonica cultivar-group)			
OC	Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Euphorbiidae; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Orzyeae; Orzyza.			
OX	Orzyza sativa L.			
RA	Salzberg S.E., Utterback T.R., Fieldblyum T.V., Blunt S., Pai G., Tsitrkin T., Rigs F., Hsiao J., Zissmann V., Blunt S., Utterback T.R., Fieldblyum T.V., Blunt S., Pai G., Quackenbush J., White O., Fraser C.M.;			
RA	Yuan Q., Ouyang S., Liu J., Moffat K.S., Hill J.N., Gansberger K., Bremer M., Burgess S., Hance M., Sivartsbey M., Buell C.R., Buell C.R., Hsiao J., Zissmann V., Blunt S., Pai G., Tsitrkin T., Rigs F., Hsiao J., Zissmann V., Blunt S., Utterback T.R., Fieldblyum T.V., Blunt S., Pai G., Quackenbush J., White O., Fraser C.M.;			
RA	Orzya sativa chromosome 10 BAC OSJNB6005J14 genomic sequence.;"			
RA	Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.			
RA	-1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.			
RA	Interpro: IPR001128; Cytochrome_P450.			
RA	PFam: PF0067; P450_1.			
RA	AC074232; AAM12483_1; -.			
RA	Gramene: QSTS6;			
RA	Interpro: IPR001128; Cytochrome_P450.			
RA	Heme; Monooxygenase; Oxidoreductase.			
RA	515 AA; 58129 MW; B83467EE81E0E85D CRC64;			
RA	SEQUENCE			
RA	5			
RA	5 GFSFCFSQIYGVYGNVTFHVPSPNVLKEYPLKEVWPKQDKVAELNESEFRAFSSR 58			
RA	61 GIVTC----YGMIGNTEDRTPS--MYEYIWIK----ENREAKVVSSE 98			
RA	61 GIVTC----YGMIGNTEDRTPS--MYEYIWIK----ENREAKVVSSE 98			
RA	Q8756	PRELIMINARY;	PRT;	562 AA.
RA	Q8756;			
RA	01-OCT-2000 (TREMBLrel. 15, Created)			
RA	01-OCT-2000 (TREMBLrel. 15, Last sequence update)			
RA	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
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RA	GN VC0184.			
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RA	OC NCBI_TAXID=666;			
RA	OX NCBI_TAXID=666;			
RA	RN [1]			
RA	RP SEQUENCE FROM N.A.			
RA	RC STRAIN=EL TOR NIE961 / Serotype: O1;			
RA	RC MEDLINE=204106833; PubMed=10952301;			
RA	RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L., Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Mayamensingh L.A., Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D., Erau Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P., McPoirier L., Utterback T., Fleischmann R.D., White O., Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C., Fraser C.M.			
RA	RT A sequence of both chromosomes of the cholera pathogen Vibrio cholerae.;"			
RA	RT DR AF004108; AAF93360_1; -.			
RA	RT DR TIGR; VC0184; -.			
RA	RT DR Hypothetical protein; Complete Proteome.			
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RA	RA Query Match 19.4%; Score 63.5%; DB 16; Length 562;			
RA	RA Best Local Similarity 27.8%; Pred. No. 27; Gaps 2;			
RA	RA Matches 15; Conservative 9; Mismatches 13; Indels 17; Gaps 2;			
RA	RA Q8756	PRELIMINARY;	PRT;	515 AA.
RA	RA AC Q8756;			
RA	RA DT 01-JUN-2002 (TREMBLrel. 21, Created)			
RA	RA DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)			
RA	RA DE Cytochrome P450-like protein.			
RA	RA GN OSB005J14.			
RA	RA OC			
RA	RA OC			
RA	RA OX			

RESULT 14

RESULT 15

Result No.	Score	Query	Match	Length	DB	ID	Description
1	327	100.0	240	1	US-07-940-861-12		Sequence 12, Appl
2	327	100.0	240	1	US-08-459-512-12		Sequence 12, Appl
3	327	100.0	240	2	US-08-459-517-12		Sequence 12, Appl
4	327	100.0	240	2	US-08-460-532-12		Sequence 12, Appl
5	327	100.0	240	3	US-08-466-465-4		Sequence 4, Appl
6	327	100.0	240	5	PCT-US92-02050-12		Sequence 12, Appl
7	327	100.0	240	6	5185441-36		Patent No. 5185441
8	327	100.0	240	6	5223394-4		Sequence 10, Appl
9	327	100.0	240	6	5223394-6		Patent No. 5223394
10	327	100.0	250	1	US-07-940-861-10		Sequence 10, Appl
11	327	100.0	250	1	US-08-459-512-10		Sequence 10, Appl
12	327	100.0	250	2	US-08-459-557-10		Sequence 10, Appl
13	327	100.0	250	2	US-08-460-532-10		Sequence 2, Appl
14	327	100.0	250	3	US-08-466-465-2		Sequence 10, Appl
15	327	100.0	250	5	PCT-US92-02050-10		Patent No. 5223394
16	327	100.0	250	6	5223394-1		Patent No. 5185441
17	327	100.0	251	6	5185441-38		Sequence 43, Appl
18	327	100.0	347	1	US-07-940-861-43		Sequence 43, Appl
19	327	100.0	347	1	US-08-459-512-43		Sequence 43, Appl
20	327	100.0	347	2	US-08-459-557-43		Sequence 43, Appl
21	327	100.0	347	2	US-08-460-532-43		Sequence 8, Appl
22	327	100.0	347	3	US-08-466-465-8		Sequence 5, Appl
23	327	100.0	347	5	PCT-US92-02050-43		Sequence 5, Appl
24	316	96.6	77	1	US-07-940-861-45		Sequence 5, Appl
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ALIGNMENTS						
RESULT 1						
US-07-940-861-12						
Sequence 12, Application US/07940861						
Patent No. 5185441						
GENERAL INFORMATION:						
APPLICANT: BIOPEN, INC.						
APPLICANT: WALLNER, Barbara P.						
APPLICANT: MILLER, Glenn T.						
APPLICANT: ROSA, Margaret D.						
TITLE OF INVENTION: CD2-BINDING DOMAIN OF LYMPHOCYTE						
TITLE OF INVENTION: FUNCTION ASSOCIATED ANTIGEN 3						
NUMBER OF SEQUENCES: 43						
CORRESPONDENCE ADDRESS:						
ADDRESSEE: Fish & Neave						
STREET: 875 Third Avenue						
CITY: New York						
STATE: New York						
COUNTRY: U.S.A.						
ZIP: 10022-6250						
COMPUTER READABLE FORM:						
MEDIUM TYPE: Floppy disk						
COMPUTER: IBM PC compatible						
OPERATING SYSTEM: PC-DOS/MS-DOS						
SOFTWARE: Patient Release #1.0, Version #1.25						
CURRENT APPLICATION DATA:						
APPLICATION NUMBER: US/07/940,861						
FILING DATE: 21-OCT-1992						
CLASSIFICATION: 514						
PRIOR APPLICATION DATA:						
APPLICATION NUMBER: PCT/US92/02050						
FILING DATE: 12-MAR-1992						
PRIOR APPLICATION DATA:						
APPLICATION NUMBER: US 07/667,971						
FILING DATE: 12-MAR-1991						
PRIOR APPLICATION DATA:						
APPLICATION NUMBER: US 07/770,967						
FILING DATE: 07-OCT-1991						
ATTORNEY/AGENT INFORMATION:						
NAME: HALEY, James F., Jr.						
REGISTRATION NUMBER: 27,794						
REFERENCE/DOCKET NUMBER: B151CIP2						
TELECOMMUNICATION INFORMATION:						
TELEPHONE: (212)715-0600						
TELEFAX: (212)715-0673						
TELELEX: 14-8567						
INFORMATION FOR SEQ ID NO: 12:						
SEQUENCE CHARACTERISTICS:						
LENGTH: 240 amino acids						
TYPE: amino acid						
TOPOLOGY: linear						

MOLECULE TYPE: protein

US-07-940-861-12

Query Match Score 327; DB 1; Length 240;  
Best Local Similarity 100.0%; Pred. No. 1.1e-34;  
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 20 LHCQGFISCFSCFQQIYGVYGNVTFHVPNSVPLKEVLWKKQDKVVAELENSEFRAFFSKN 79

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Db 20 LHCQGFISCFSCFQQIYGVYGNVTFHVPNSVPLKEVLWKKQDKVVAELENSEFRAFFSKN 79

Qy 61 R 61

Db 80 R 80

RESULT 3  
US-08-459-557-12

Sequence 12, Application US/08459657  
Patent No. 5944111

GENERAL INFORMATION:

APPLICANT: BIOPHARM, INC.  
APPLICANT: WALLNER, Barbara P.  
APPLICANT: MILLER, Glenn T.  
APPLICANT: ROSA, Margaret D.

TITLE OF INVENTION: CD2-BINDING DOMAIN OF LYMPHOCYTE FUNCTION ASSOCIATED ANTIGEN 3

NUMBER OF SEQUENCES: 43

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Neave  
STREET: 875 Third Avenue  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10022-6550

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/459,657  
FILING DATE: 02-JUN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 12-MAR-1992  
FILING DATE: 12-MAR-1991

APPLICATION NUMBER: US/07/770,967  
FILING DATE: 07-OCT-1991

ATTORNEY/AGENT INFORMATION:

NAME: HALEY, James F., Jr.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: B151CIP2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)715-0600  
TELEFAX: (212)715-0673  
TELEX: 14-8367

INFORMATION FOR SEQ ID NO: 12:

NAME: HALEY, James F., Jr.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: B151CIP2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)715-0600  
TELEFAX: (212)715-0673  
TELEX: 14-8367

SEQUENCE CHARACTERISTICS:

LENGTH: 240 amino acids  
TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

Query Match Score 327; DB 1; Length 240;  
Best Local Similarity 100.0%; Pred. No. 1.1e-34;  
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 LHCQGFISCFSCFQQIYGVYGNVTFHVPNSVPLKEVLWKKQDKVVAELENSEFRAFFSKN 79

Qy 61 R 61

Db 80 R 80

GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: October 7, 2003, 16:52:18 ; Search time: 12.7083 Seconds

(without alignments)  
759,422 Million cell updates/sec

Title: US-09-730-465-2\_COPY\_20\_80

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Gapext 0.0 , Gapext 0.5

Searched: 587654 seqs, 158212981 residues

Total number of hits satisfying chosen parameters: 587654

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%

Maximum Match 100%

Listing first 45 summaries

Published Applications AA: \*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Databases :

Sequence 2, Appli



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 7, 2003, 11:24:22 ; Search time 81 Seconds

(without alignments)  
31.353 Million cell updates/sec

Title: US-09-730-465-2\_COPY\_50\_65  
Sequence: 1 PLKEVLMKKQDKVVA 16

Scoring table: BLOSUM62

Gapext: 0.5

Searched: 1107663 seqs, 158726573 residues

total number of hits satisfying chosen parameters:

360314

Minimum DB seq length: 0  
Maximum DB seq length: 16

Post-processing: Minimum Match 100%

Maximum Match 100%

Listing first 45 summaries

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Human peptide #179  
Pair 3 Pep 5 immun  
Nociceptin-like im  
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Amino acid sequenc  
Gene delivery pla  
Nociceptin-like pe  
Nociceptin-like pe  
Nociceptin-like pe  
Nociceptin-like pe  
Human Peptide #195  
Human protein frag  
Gene delivery pla  
Yes-encoded oncopr  
Anti-fungal peptid  
Protein S - C4BP b  
CTLA-2 beta frigme  
Synthatic cytotoxi  
Human gene 7 encod

10 34 40.5 15 24 ABR33624  
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17 32 38.1 14 22 AAM8523  
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19 31 36.9 8 23 AAU76075  
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24 31 36.9 12 23 AAU76099  
25 31 36.9 12 23 AAU76102  
26 31 36.9 12 23 AAU76105  
27 31 36.9 12 23 AAU76107  
28 31 36.9 12 23 AAU76112  
29 31 36.9 13 23 AAU76111  
30 31 36.9 14 18 AAU76446  
31 31 36.9 14 22 AAM86920  
32 31 36.9 14 22 AAM00706  
33 31 36.9 15 23 ABP53305  
34 31 36.9 16 21 AAY52664  
35 30 35.7 8 18 AAN44604  
36 30 35.7 8 20 RAY00581  
37 30 35.7 8 22 AAB65505  
38 30 35.7 9 17 AAU04048  
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40 30 35.7 9 20 AAY00539  
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42 30 35.7 14 14 AAR31887  
43 30 35.7 16 15 AAR7955  
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#### ALIGNMENTS

RESULT 1  
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ID AAE23846 standard; peptide: 16 AA.

XX

XX

XX

XX

XX

Human zsig33-gamma peptide # 2.

10-SEP-2002 (First entry)

Human zsig33-gamma peptide # 2.

Human; zsig33-like peptide; gastric contractility; nutrient uptake; growth hormone; digestive enzyme; restorative therapy; gene protein therapy; gastrointestinal; endocrine; anabolic.

Homo sapiens.

US2002055156 A1.

09-MAY-2002.

XX

WPI; 2002-443750/47.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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3	36	42.9	16	23 AAE15891	Human zsig33-gamma
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5	35	41.7	15	23 AAE15898	Fragment of T-serg
6	35	41.7	15	23 ABP53304	tissue anion trans
7	34	40.5	10	21 AAY65683	Human c-Erb-A nuc1
8	34	40.5	15	23 AAE23848	Human zsig33-gamma
9	34	40.5	15	23 AAE15893	Human zsig33-gamma

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

25 ZSIG33-Like peptides and polynucleotides, useful for modulating gastric contractility, nutrient uptake, growth hormones and/or secretion of digestive/pancreatic enzymes and hormones -

Claim 5, Page 30: 34pp; English.

Claim 5; Page 30; 34pp; English.

The invention relates to zsig33-like peptides and their corresponding nucleic acids and methods for modulating gastric contractility, nutrient uptake, growth hormones, secretion of digestive enzymes and hormones and diagnosis/treatment of diseases associated with inappropriate ZSIG33 expression. The nucleic acids of the invention and their complements are used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which patients may be in need of restorative therapy. The ZSIG33 peptides are used as anti-modulators of ZSIG33 and in assays to identify modulators of ZSIG33 expression and activity. The anti-ZSIG33 antibody and antagonists are used to down regulate expression and activity. The anti-ZSIG33 antibodies are also used as diagnostic agents for detecting the presence of ZSIG33 in samples (e.g., by enzyme linked immunosorbent assay (ELISA). The peptides and nucleic acids of the invention are used to modulate gastric contractility, nutrient uptake, growth hormones, secretion of digestive enzymes and hormones, and/or secretion of enzymes and/or hormones in the pancreas. zsig33-like DNA is used in gene therapy and zsig33-like peptide is used in protein therapy. The present sequence is human zsig33-like peptide, zsig33-gamma peptide.

Claim 5; Page 30; 34pp; English.

The invention relates to zsig33-like peptides and their corresponding nucleic acids and methods for modulating gastric contractility, nutrient uptake, growth hormones, secretion of digestive enzymes and hormones. The sequences of the invention are used in the prevention, diagnosis and treatment of diseases associated with inappropriate ZSIG33 expression. The nucleic acids of the invention and their complements are used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which patients may be in need of restorative therapy. The ZSIG33 peptides are used as antigens in the production of antibodies against ZSIG33 and in assays to identify modulators of ZSIG33 expression and activity. The anti-ZSIG33 antibodies and antagonists are used to down regulate expression and activity. The anti-ZSIG33 antibodies are also used as diagnostic agents for detecting the presence of ZSIG33 in samples (e.g. by enzyme linked immunosorbent assay (ELISA)). The peptides and nucleic acids of the invention are used to modulate gastric contractility, nutrient uptake, growth hormones, the secretion of digestive enzymes and hormones, and/or secretion of enzymes and/or hormones in the pancreas. zsig33-like DNA is used in gene therapy and zsig33-like peptide is used in protein therapy. The present sequence is human zsig33-like peptide, zsig33-gamma peptide.

Sequence	16 AA;
Identity	42.9%;
Local Similarity	33.3%;
Mismatches	5;
Conservative	7;
Mismatches	3;
Pred. No.	91;
Indels	0;
Gaps	0;
Length	16;

AAE23847

Human zsig33-gamma peptide #3.

Human; zsig33-like peptide; gastric contractility; nutrient uptake; growth hormone; digestive enzyme; restorative therapy; gene therapy; protein therapy; gastrointestinal; endocrine; anabolic.

Homo sapiens.

US2002051556-A1.

09-MAY-2002.

10-MAY-2001; 2001US-0853253.

11-MAY-2000; 2000US-203300P.

(JASP/ ) JASPERS S R.  
(SHEP/ ) SHEPPARD P O.  
(DEIS/ ) DEISHER T A.  
(BISH/ ) BISHOP P D.

Jaspers SR, Sheppard PO, Deisher TA, Bishop PD;

WPI; 2002-443750/4.

Scoring table:	BLOSUM62	84	1	PIKEVLWKQDKVVAE 16	Scoring table: Gapop 10.0 , Gapext 0.5	Scoring table: Gapop 10.0 , Gapext 0.5	Scoring table: Gapop 10.0 , Gapext 0.5	Scoring table: Gapop 10.0 , Gapext 0.5
Searched:	127863 seqs, 47026705 residues	872			Total number of hits satisfying chosen parameters: 872			
Minimum DB seq length:	0				Minimum DB seq length: 0			
Maximum DB seq length:	16				Maximum DB seq length: 16			
Post-Processing:	Maximum Match 0%				Post-Processing: Maximum Match 0%			
Database:	SwissProt_41:*				Database: SwissProt_41:*			
Result No.	Score	Query Match Length	DB ID	Description	Result No.	Score	Query Match Length	DB ID
1	23	27.4	15	MALT_BACTQ	1	23	27.4	P8072 bacillus th
2	21	25.0	13	NO40_PEA	2	21	25.0	P55599 Pisum sativ
3	21	25.0	13	NO40_VICSA	3	21	25.0	P55961 Vicia sativ
4	21	25.0	13	RPOC_NYCGA	4	21	25.0	P47716 mycoplasma
5	21	25.0	14	MAST_PARID	5	21	25.0	P42716 parapolybia
6	21	25.0	14	MAST_POLJA	6	21	23.8	P01517 polistes ja
7	20	23.8	12	UR2B_CATCO	7	20	23.8	P04559 catostomus
8	20	23.8	12	UR2B_CYPCA	8	20	23.8	P04761 cyprinus ca
9	20	23.8	12	UR2B_POLSP	9	20	23.8	P81022 Sicyodon sp
10	20	23.8	14	SMS1_MYOSC	10	20	23.8	P20750 myoxocephal
11	20	23.8	14	SMS_ALMI	11	20	23.8	P31885 alligator m
12	18.5	22.0	14	MAST_YESBA	12	18	21.4	P12154 vespa basal
13	18	21.4	10	SP1_HALRO	13	18	21.4	Q10997 halocynthia
14	18	21.4	11	LPW_THBTH	14	18	21.4	P05674 thermus the
15	18	21.4	12	NO40_SESRO	15	18	21.4	P04469 sesbania ro
16	18	21.4	15	PGKH_PHYPA	16	18	21.4	P80559 physcomitre
17	18	21.4	16	FLBA_MELME	17	18	21.4	P14456 meles meles
18	18	21.4	16	FIBA_MDSVI	18	18	21.4	P14458 mustela vis
19	17	20.2	7	WWA2_ACHFU	19	17	20.2	P35920 achatina fu
20	17	20.2	7	WWA3_ACHFU	20	17	20.2	P35921 achatina fu
21	17	20.2	9	LPCA_STAAU	21	17	20.2	P36584 staphylococ
22	17	20.2	11	CEP1_ACHFU	22	17	20.2	P22790 achatina fu
23	17	20.2	11	Q2OA_COMTE	23	17	20.2	P80464 comamas t
24	17	20.2	12	NO40_LOTJA	24	17	20.2	P02246 lotus japon
25	17	20.2	12	RS19_CLYEP	25	17	20.2	Q46190 clover yell
26	17	20.2	12	RS19_TOBBP	26	17	20.2	Q56551 tomato big
27	17	20.2	12	UR2A_CATCO	27	17	20.2	P04558 catostomus
28	17	20.2	12	UR2_GILMI	28	17	20.2	P01147 gillichthys
29	17	20.2	12	UR2_SCYCA	29	17	20.2	P35490 scylliorhinu
30	17	20.2	13	AU11_LITRA	30	17	20.2	P82386 1itoria ran
31	17	20.2	13	AU12_LITRA	31	17	20.2	P82387 1itoria ran
32	17	20.2	14	RS19_PRUAP	32	17	20.2	Q44160 prunus armen
33	17	20.2	15	C1QA_RAT	33	17	20.2	P31720 rattus norv

ALIGNMENTS								
RESULT 1								
MALT_BACTQ								
ID	MALT_BACTQ							
AC	P80072;							
DT	01-AUG-1992 (Rel. 23, Created)							
DR	01-AUG-1992 (Rel. 23, Last sequence update)							
DT	01-DEC-1992 (Rel. 24, Last annotation update)							
DE	Maltase (EC 3.2.1.20) (Alpha-glucosidase I) (Fragment).							
OS	Bacillus thermomyloliquefaciens.							
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.							
NCBI_TAXID	1425;							
OX								
RN	[1]							
RP								
SEQUENCE.								
STRAIN	KP1071 / FERM P8477;							
MEDLINE	92109510; PubMed-155585;							
RA	Suzuki Y., Yonezawa K., Hattori M., Takii Y.;							
RT	"Assignment of <i>Bacillus thermomyloliquefaciens</i> KP1071 alpha-glucosidase I to an exo-alpha-1,4-glucosidase, and its striking similarity to bacillary oligo-1,6-glucosidases in N-terminal sequence and in structural parameters calculated from the amino acid composition."							
RT	Bur. J. Biochem. 205:249-256(1992).							
RT	-1- CATALYTIC ACTIVITY: Hydrolysis of terminal, non-reducing 1,4-linked D-glucose residues with release of D-glucose.							
CC								
CC	-1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO KNOWN AS THE ALPHA-AMYLASE FAMILY.							
CC	PIR: S21240.							
KW	Hydrolase; Glycosidase.							
FT	NON_TER 15 15							
SEQUENCE	SEQUENCE 15 AA; 1929 MW;							
CC	Query Match Score 23; DB 1; Length 15;							
CC	Best Local Similarity 37.5%; Mismatches 3; Conservative 2; Indels 0; Gaps 0;							
QY	2 IKEVLWKK 9							
QY	2 IKEVLWKK 9							
DB	1 MCKAWWKE 8							
DB	1 MCKAWWKE 8							
REQU2								
NO40_PEA								
ID	NO40_PEA							
AC	P55959;							
DT	01-NOV-1997 (Rel. 35, Created)							
DT	01-NOV-1997 (Rel. 35, Last sequence update)							
DE	Early nodulin 40.							
GN	Plum sativum (Garden pea).							
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; Papilionoideae; Vicieae; Rosidae; eurotids I; Fabales; Fabaceae; core eudicots; Pisum.							
OC	NCBI_TAXID-3888;							
RN	[1]							
RP	SEQUENCE FROM N.A.							

STRAIN=cv. Sparkle; TISSUE=Root nodules;  
 RX MEDLINE=950121; PubMed=7948896;  
 RA Matvienko M., van de Sande K., Yang W.C., van Kammen A., Bisseling T.,  
 RA Franssen H.J.;  
 RA "Comparison of soybean and pea ENOD40 cDNA clones representing genes  
 expressed during both early and late stages of nodule development.";  
 RT Plant Mol. Biol. 26:477-493 (1994).  
 RL -!  
 CC FUNCTION: MODULATES THE ACTION OF AUXIN, AND MAY FUNCTION AS PLANT  
 GROWTH REGULATOR THAT ALTERS PHYTOHORMONE RESPONSES (BY  
 SIMILARITY).  
 CC GROWTH REGULATOR THAT ALTERS PHYTOHORMONE RESPONSES (BY  
 SIMILARITY).  
 CC DEVELOPMENTAL STAGE: EXPRESSED IN THE EARLY STAGES OF THE NODULE  
 CC NODULATION.  
 CC DR EMBL: X81064; -; NOT\_ANNOTATED\_CDS.  
 CC KW NODULATION.  
 CC SQ SEQUENCE 13 AA; 156 MW; 3C695566BD8A26C3 CRC64;  
 CC Query Match 25.0%; Score 21; DB 1; Length 13;  
 CC Best Local Similarity 37.5%; Pred. No. 1.5e+03;  
 CC Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
 CC QY 2 LKEVINK 9  
 CC :| :| :|  
 CC Db 1 MKFLCWQK 8

RESULT 3  
 NO40\_YICSA  
 ID NO40\_YICSA  
 AC P55951;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Early nodulin 40.  
 OS Vicia sativa (Spring vetch) (Tare).  
 OC Eukaryota; Viridiplantae; Strptophyta; Embryophyta; tracheophyta;  
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Vicia.  
 OC NBI\_TAXID=3908;  
 RN 1  
 RN SEQUENCE FROM N.A.  
 RC TISSUE=Root nodules;  
 RX MEDLINE=96011756; PubMed=7548828;  
 RA Vijn I., Yang W.-C., Paliisgaard N., Oestergaard Jensen E.,  
 RA van Kammen A., Bisseling T.;  
 RA "VSENOD5, VSENOD12 and VSENOD40 expression during Rhizobium-induced  
 nodule formation on Vicia sativa roots.";  
 RT Plant Mol. Biol. 28:1111-1119 (1995).  
 RL -!  
 CC FUNCTION: MODULATES THE ACTION OF AUXIN, AND MAY FUNCTION AS PLANT  
 GROWTH REGULATOR THAT ALTERS PHYTOHORMONE RESPONSES (BY  
 SIMILARITY).  
 CC DEVELOPMENTAL STAGE: EXPRESSED DURING RHIZOBIUM-INDUCED NODULE  
 FORMATION. IN 4-DAY OLD NODULES IT IS FOUND IN ALL THE CELLS OF  
 THE CENTRE OF THE NODULE PRIMORDIUM AND ALSO OCCURS IN THE REGION  
 OF THE ROOT PERICYCLE FACING THE NODULE PRIMORDIUM. AT DAY 5,  
 EXPRESSION IS SEEN IN THE COMPLETE CENTRAL TISSUE. AT DAY 20  
 EXPRESSED IN THE COMPLETE PREFIXATION ZONE II, AND IN THE BROWNL  
 PART OF THIS ZONE IT IS FOUND ONLY IN THE INFECTED CELLS BUT NOT  
 IN THE UNINFECTED CELLS. AT THE TRANSITION OF PREFIXATION ZONE II  
 INTO INTERZONE II-III EXPRESSION DECREASES IN THE INFECTED CELLS.  
 CC IN THE FIXATION ZONE III EXPRESSION IS INDUCED IN THE UNINFECTED  
 CELLS AND IN THE PROXIMAL PART OF THIS ZONE IT IS UNDETECTABLE.  
 CC PRESENT AT HIGH LEVELS IN THE PERICYCLE OF THE NODULE VASCULAR  
 CC BUNDLE.

CC STRAIN=cv. Sparkle; TISSUE=Root nodules;  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement. (See http://www.isb-sib.ch/announce/  
 CC or send an email to license@isb-sib.ch).  
 CC EMBL; X83683; CAB37926.1; -.  
 CC PIR; S60046; S60046.  
 CC KW Nodulation.  
 CC SQ SEQUENCE 13 AA; 1531 MW; 3C6953C4BD8A26C3 CRC64;  
 CC Query Match 25.0%; Score 21; DB 1; Length 13;  
 CC Best Local Similarity 37.5%; Pred. No. 1.5e+03;  
 CC Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
 CC QY 2 LKEVINK 9  
 CC :| :| :|  
 CC Db 1 MKFLCWQK 8

RESULT 4  
 RP0C\_MYCGA  
 ID RP0C\_MYCGA  
 AC P47716;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE DNA-directed RNA polymerase beta' chain (EC 2.7.7.6) (transcriptase  
 DE beta' chain) (RNA polymerase beta' subunit) (Fragment).  
 GN RP0C.  
 OS Mycoplasma gallisepticum.  
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.  
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=A596var.;  
 RA Skamrov A.V., Feoktistova E.S., Gol'dman M.A., Feoktistova E.S.,  
 RA Bibilashvili R.S.;  
 RL Submitted (XXX-1995) to the EMBL/GenBank/DDJB databases.  
 CC -!  
 CC FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION  
 CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS  
 CC SUBSTRATES  
 CC -!  
 CC CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +  
 CC (RNA) (N).  
 CC -!  
 CC SUBUNIT: THE ENZYME CONSISTS OF THE SIGMA CHAIN AND THE CORE  
 CC ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA CHAIN, AND 1  
 CC BETA' CHAIN.  
 CC -!  
 CC SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.  
 CC DR L38402; AAB40952.1; -.  
 CC KW RNA-directed RNA polymerase; Transcriptase.  
 CC SQ SEQUENCE 13 AA; 1530 MW; 4BEC27C7480D4333 CRC64;  
 CC Query Match 25.0%; Score 21; DB 1; Length 13;  
 CC Best Local Similarity 66.7%; Pred. No. 1.5e+03;  
 CC Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;  
 CC QY 8 KKNDK 13  
 CC :| :| :|  
 CC Db 6 KKNNNK 11

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Database : SPTREMBL_23;*							
1: sp_archaea:*							
2: sp_bacteria:*							
3: sp_fungi:*							
4: sp_human:*							
5: sp_invertebrate:*							
6: sp_mammal:*							
7: sp_mhc:*							
8: sp_organelle:*							
9: sp_phage:*							
10: sp_plant:*							
11: sp_rabbit:*							
12: sp_virus:*							
13: sp_vertebrate:*							
14: sp_unclassified:*							
15: sp_rvirus:*							
16: sp_bacteriaph:*							
17: sp_archeap:*							
Run on: October 7, 2003, 11:25:43 ; Search time 92 Seconds							
(without alignments)							
44.879 Million cell updates/sec							
Perfect score: 84							
Sequence: 1 PLKEVILWKQKDKVAE 16							
Scoring table: BLOSUM62							
Gapop 10.0 , Gapext 0.5							
Total number of hits satisfying chosen parameters: 4022							
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Maximum DB seq length: 16							
Post-processing: Minimum Match 0%							
Maximum Match 100%							
Listing first 45 summaries							
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6: sp_mammal:*							
7: sp_mhc:*							
8: sp_organelle:*							
9: sp_phage:*							
10: sp_plant:*							
11: sp_rabbit:*							
12: sp_virus:*							
13: sp_vertebrate:*							
14: sp_unclassified:*							
15: sp_rvirus:*							
16: sp_bacteriaph:*							
17: sp_archeap:*							
Run on: October 7, 2003, 11:25:43 ; Search time 92 Seconds							
(without alignments)							
44.879 Million cell updates/sec							
Perfect score: 84							
Sequence: 1 PLKEVILWKQKDKVAE 16							
Scoring table: BLOSUM62							
Gapop 10.0 , Gapext 0.5							
Total number of hits satisfying chosen parameters: 4022							
Minimum DB seq length: 0							
Maximum DB seq length: 16							
Post-processing: Minimum Match 0%							
Maximum Match 100%							
Listing first 45 summaries							
Database : SPTREMBL_23;*							
1: sp_archaea:*							
2: sp_bacteria:*							
3: sp_fungi:*							
4: sp_human:*							
5: sp_invertebrate:*							
6: sp_mammal:*							
7: sp_mhc:*							
8: sp_organelle:*							
9: sp_phage:*							
10: sp_plant:*							
11: sp_rabbit:*							
12: sp_virus:*							
13: sp_vertebrate:*							
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17: sp_archeap:*							
Run on: October 7, 2003, 11:25:43 ; Search time 92 Seconds							
(without alignments)							
44.879 Million cell updates/sec							
Perfect score: 84							
Sequence: 1 PLKEVILWKQKDKVAE 16							
Scoring table: BLOSUM62							
Gapop 10.0 , Gapext 0.5							
Total number of hits satisfying chosen parameters: 4022							
Minimum DB seq length: 0							
Maximum DB seq length: 16							
Post-processing: Minimum Match 0%							
Maximum Match 100%							
Listing first 45 summaries							
Database : SPTREMBL_23;*							
1: sp_archaea:*							
2: sp_bacteria:*							
3: sp_fungi:*							
4: sp_human:*							
5: sp_invertebrate:*							
6: sp_mammal:*							
7: sp_mhc:*							
8: sp_organelle:*							
9: sp_phage:*							
10: sp_plant:*							
11: sp_rabbit:*							
12: sp_virus:*							
13: sp_vertebrate:*							
14: sp_unclassified:*							
15: sp_rvirus:*							
16: sp_bacteriaph:*							
17: sp_archeap:*							
Run on: October 7, 2003, 11:25:43 ; Search time 92 Seconds							
(without alignments)							
44.879 Million cell updates/sec							
Perfect score: 84							
Sequence: 1 PLKEVILWKQKDKVAE 16							
Scoring table: BLOSUM62							
Gapop 10.0 , Gapext 0.5							
Total number of hits satisfying chosen parameters: 4022							
Minimum DB seq length: 0							
Maximum DB seq length: 16							
Post-processing: Minimum Match 0%							
Maximum Match							



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 7, 2003, 11:27:28 ; Search time 16 Seconds  
(without alignments)  
42.311 Million cell updates/sec

Title: US-09-730-465-2\_COPY\_50\_65  
Perfect score: 84  
Sequence: 1 PLKEV7LWKQDKYTAE 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 133293

Minimum DB seq length: 0

Maximum DB seq length: 16

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents AA:  
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3: /cgn2\_6\_ptodata/1/iaa/6A\_COMB.pep:  
4: /cgn2\_6\_ptodata/1/iaa/6B\_COMB.pep:  
5: /cgn2\_6\_ptodata/1/iaa/PCrTUS.Comb.pep:  
6: /cgn2\_6\_ptodata/1/iaa/backtlesi.pep:  
\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	42	50.0	7	6	5185441-12		Patent No. 5185441
2	31	36.9	10	4	US-09-050-811-5		Sequence 5, Appli
3	31	36.9	15	4	US-09-050-811-6		Sequence 6, Appli
4	31	36.9	15	4	US-09-050-811-11		Sequence 11, Appli
5	30	35.7	8	2	US-08-6221259A205		Sequence 205, APP
6	30	35.7	9	5	PCT-US95-09262-163		Sequence 163, APP
7	30	35.7	14	1	US-07-907-190-13		Sequence 163, APP
8	30	35.7	16	2	US-08-485-937-11		Sequence 13, APP
9	30	35.7	16	2	US-08-373-215-11		Sequence 11, APP
10	30	35.7	16	5	PCT-US93-06552-11		Sequence 11, APP
11	30	35.7	15	1	US-08-311-611-116		Sequence 116, APP
12	29	34.5	15	1	US-08-372-783-116		Sequence 116, APP
13	29	34.5	15	1	US-08-372-105-116		Sequence 116, APP
14	29	34.5	15	1	US-08-306-473A-116		Sequence 116, APP
15	29	34.5	15	2	US-08-6221-803-101		Sequence 101, APP
16	29	34.5	15	2	US-08-485-445A-116		Sequence 116, APP
17	29	34.5	15	3	US-08-119-263-116		Sequence 116, APP
18	29	34.5	15	3	US-08-657-162-116		Sequence 116, APP
19	29	34.5	15	3	US-09-224-480-116		Sequence 116, APP
20	29	34.5	15	3	US-09-217-210-101		Sequence 101, APP
21	29	34.5	15	5	PCT-US95-00498-116		Sequence 116, APP
22	29	34.5	15	5	PCT-US95-00655-116		Sequence 116, APP
23	29	34.5	15	5	PCT-US95-160-1		Sequence 116, APP
24	28	33.3	11	4	US-09-025-596-23		Sequence 1, Appli
25	28	33.3	14	4	US-09-07985-691-17		Sequence 23, Appli
26	28	33.3	15	1	US-09-223-139-32		Sequence 17, Appli
27	33.3						Sequence 32, Appli

#### ALIGNMENTS

RESULT 1  
5185441-12

; Patent No. 5185441  
; APPLICANT: WALINGER, BARBARA P.; HESSONS, CATHERINE  
; TITLE OF INVENTION: DNA SEQUENCES, RECOMBINANT DNA  
; MOLECULES AND PROCESSES FOR PRODUCING PI-LINKED LYMPHOCYTE  
; FUNCTION ASSOCIATED ANTIGEN-3  
; NUMBER OF SEQUENCES: 41  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US-07/237,309  
; SEQ ID NO:12:  
; FILING DATE: 26-AUG-1988  
; LENGTH: 7  
5185441-12

Query 7 WRKQDK  
Best Local Similarity 50.0%; Score 42; DB 6; Length 7;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

WRKQDK 13  
WRKQDK 7

RESULT 2  
US-09-050-811-5

; Sequence 5, Application US/09050811  
; Patent No. 6387700

; GENERAL INFORMATION:  
APPLICANT: Rice, Kevin G.  
APPLICANT: Wadhwa, Manpreet S.  
TITLE OF INVENTION: Peptides for Gene Delivery  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLIN & CARROLL, LLP  
STREET: 220 Montromery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104

; COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/050,811  
FILING DATE: 30-MAR-1998  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:

NAME: Carroll, Peter G.  
 REGISTRATION NUMBER: 32,837  
 TELECOMMUNICATION INFORMATION:  
 TELEFAX: 415/705-8410  
 INFORMATION FOR SEQ ID NO: 5:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 10 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: not relevant  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 FEATURE:  
 NAME/KEY: Binding-site  
 LOCATION: 1  
 OTHER INFORMATION: /note= "The residue at this position is bound to an Alkaloid by a Sulfide."  
 US-09-050-811-5

Query Match 36.9%; Score 31; DB 4; Length 10;  
 Best Local Similarity 71.4%; Pred. No. 81;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 7 WKKQDK 13  
 Db 1 1 : 1  
 2 WKKKKK 8

RESULT 4  
 US-09-050-811-11  
 Sequence 11, Application US/09050811  
 GENERAL INFORMATION:  
 APPLICANT: Rice, Kevin G.  
 ATTORNEY/AGENT INFORMATION:  
 TITLE OF INVENTION: Peptides for Gene Delivery  
 NUMBER OF SEQUENCES: 11  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: MEDLEN & CARROLL, LLP  
 STREET: 220 Montgomery Street, Suite 2200  
 CITY: San Francisco  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 94104

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/050,811  
 FILING DATE: 30-MAR-1998  
 CLASSIFICATION: 514  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Carroll, Peter G.  
 REGISTRATION NUMBER: 32,837  
 REFERENCE/DOCKET NUMBER: UM-03314  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415/705-8410  
 TELEFAX: 415/397-8338  
 INFORMATION FOR SEQ ID NO: 11:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 15 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: not relevant  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-09-050-811-11

Query Match 36.9%; Score 31; DB 4; Length 15;  
 Best Local Similarity 71.4%; Pred. No. 1.2e+02;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 7 WKKQDK 13  
 Db 1 1 : 1  
 2 WKKKKK 8

RESULT 5  
 US-08-921-259A-205  
 Sequence 205, Application US/08621259A  
 GENERAL INFORMATION:  
 APPLICANT: Little II, Roger G  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Lim, Edward  
 REGISTRATION NUMBER: 32,837  
 CURRENT APPLICATION DATA:  
 FILING DATE: 30-MAR-1998  
 CLASSIFICATION: 514  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Carroll, Peter G.  
 REGISTRATION NUMBER: 32,837  
 INFORMATION FOR SEQ ID NO: 6:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 15 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: not relevant  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 FEATURE:  
 NAME/KEY: Binding-site  
 LOCATION: 1  
 OTHER INFORMATION: /note= "The residue at this position is bound to an Alkaloid by a Sulfide."  
 OTHER INFORMATION: 1  
 OTHER INFORMATION: 252  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: McAndrews, Held & Malloy, Ltd.

GenCore version 5.1.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

October 7, 2003, 11:31:08 ; Search time 67 Seconds  
(without alignments)

37.762 Million cell updates/sec

Title: US-09-730-465-2\_COPY\_50\_65

Perfect score: 84

Sequence: 1\_PKEVINKKOKDKVAA 16

Scoring table: BLOSUM62

Gapext 10.0 , Gapext 0.5

Searched: 587554 seqs, 158212981 residues

Total number of hits satisfying chosen parameters: 107419

Minimum DB seq length: 16  
Maximum DB seq length: 16

Post-processing: Minimum Match 100%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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Result No.	Score	Query Match	Length	DB ID	Description
1	36	42.9	16	9 US-09-853-253-15	Sequence 15, Appl
2	36	42.9	16	9 US-09-853-253-16	Sequence 16, Appl
3	34	40.5	15	9 US-09-853-253-17	Sequence 17, Appl
4	31	36.9	8	11 US-09-882-291-63	Sequence 63, Appl
5	31	36.9	9	11 US-09-882-291-61	Sequence 61, Appl
6	31	36.9	10	12 US-10-108-844-5	Sequence 5, Appl
7	31	36.9	11	11 US-09-882-291-55	Sequence 55, Appl
8	31	36.9	12	11 US-09-882-291-35	Sequence 35, Appl
9	31	36.9	12	11 US-09-882-291-50	Sequence 50, Appl
10	31	36.9	12	11 US-09-882-291-53	Sequence 53, Appl
11	31	36.9	13	11 US-09-882-291-56	Sequence 56, Appl
12	31	36.9	15	12 US-10-108-844-6	Sequence 6, Appl
13	31	36.9	15	12 US-10-108-844-11	Sequence 11, Appl
14	30	35.7	9	9 US-09-881-490-163	Sequence 163, App
15	34.5	9	9	US-09-765-527-101	Sequence 101, Appl

#### ALIGNMENTS

RESULT 1  
US-09-853-253-15  
; Sequence 15, Application US/09853253  
; Patent No. US20020055156A1  
; GENERAL INFORMATION:  
; APPLICANT: JASPER, STEPHEN  
; APPLICANT: SHEPPARD, PAUL  
; APPLICANT: DEISHER, THERESA  
; APPLICANT: BISHOP, PAUL  
; TITLE OF INVENTION: zsig33-like Peptides  
; FILE REFERENCE: 00-30  
; CURRENT APPLICATION NUMBER: US/09/853,253  
; CURRENT FILING DATE: 2001-05-10  
; PRIOR APPLICATION NUMBER: 60/203,300  
; PRIOR FILING DATE: 2000-05-11  
; NUMBER OF SEQ ID NOS: 28  
; SEQ ID NO 15  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-09-853-253-15

RESULT 2  
US-09-853-253-16  
; Sequence 6, Application US/09853253  
; Patent No. US20020055156A1  
; GENERAL INFORMATION:  
; APPLICANT: JASPER, STEPHEN

APPLICANT: SHEPPARD, PAUL  
 APPLICANT: DELISHER, THERESA  
 APPLICANT: BISHOP, PAUL  
 TITLE OF INVENTION: Zsigt33-like Peptides  
 FILE REFERENCE: 00-30  
 CURRENT APPLICATION NUMBER: US/09/853,253  
 CURRENT FILING DATE: 2001-05-10  
 PRIOR APPLICATION NUMBER: 60/203,300  
 PRIOR FILING DATE: 2000-05-11  
 NUMBER OF SEQ ID NOS: 28  
 SOFTWARE: FastSEQ for Windows Version 3.0  
 SEQ ID NO: 16  
 LENGTH: 16  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 FEATURE: NAME/KEY: AMIDATION  
 LOCATION: (16)...(16)  
 S-09-853-253-16

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 Best Local Similarity 33.3%; Pred. No. 56;  
 Matches 5; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

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 b 2 LDILWEEAKEAPAD 16

RESULT 3  
 S-09-853-253-17  
 Sequence 17, Application US/09853253  
 Patent No. US20030055156A1  
 GENERAL INFORMATION:  
 APPLICANT: JASPERS, STEPHEN  
 APPLICANT: SHEPPARD, PAUL  
 APPLICANT: DELISHER, THERESA  
 APPLICANT: BISHOP, PAUL  
 TITLE OF INVENTION: Zsigt33-like Peptides  
 FILE REFERENCE: 00-30  
 CURRENT APPLICATION NUMBER: US/09/853,253  
 CURRENT FILING DATE: 2001-05-10  
 PRIOR APPLICATION NUMBER: 60/203,300  
 PRIOR FILING DATE: 2000-05-11  
 NUMBER OF SEQ ID NOS: 28  
 SOFTWARE: FastSEQ for Windows Version 3.0  
 SEQ ID NO: 17  
 LENGTH: 15  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 FEATURE: NAME/KEY: AMIDATION  
 LOCATION: (15)...(15)  
 S-09-853-253-17

Query Match 40.5%; Score 34; DB 9; Length 15;  
 Best Local Similarity 35.7%; Pred. No. 1e+02;  
 Matches 5; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Y 2 LKEVILWKQKDVKVA 15  
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 b 2 LDILWEEAKEAPAD 15

RESULT 4  
 S-09-882-291-63  
 Sequence 63, Application US/09882291  
 GENERAL INFORMATION:  
 APPLICANT: Zealand Pharmaceuticals A/S  
 TITLE OF INVENTION: No. US20030040472A1 Peptide Conjugates  
 FILE REFERENCE: 007-2001  
 CURRENT APPLICATION NUMBER: US/09/882,291

APPLICANT: SHEPPARD, PAUL  
 APPLICANT: DELISHER, THERESA  
 APPLICANT: BISHOP, PAUL  
 TITLE OF INVENTION: Zsigt33-like Peptides  
 FILE REFERENCE: 00-30  
 CURRENT FILING DATE: 2001-05-15  
 NUMBER OF SEQ ID NOS: 77  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO: 63  
 LENGTH: 8  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence: synthetic peptide sequen  
 US-09-882-291-63

Query Match 36.9%; Score 31; DB 11; Length 8;  
 Best Local Similarity 71.4%; Pred. No. 5.2e+05;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Y 7 WKQKDK 13  
 |:|:|:  
 b 2 WKKKKKK 8

RESULT 5  
 US-09-882-291-61  
 Sequence 61, Application US/09882291  
 Publication No. US20030040472A1  
 GENERAL INFORMATION:  
 APPLICANT: Zealand Pharmaceuticals A/S  
 TITLE OF INVENTION: No. US20030040472A1 Peptide Conjugates  
 FILE REFERENCE: 007-2001  
 CURRENT APPLICATION NUMBER: US/09/882,291  
 CURRENT FILING DATE: 2001-05-15  
 NUMBER OF SEQ ID NOS: 77  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO: 61  
 LENGTH: 9  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence: synthetic peptide sequen  
 US-09-882-291-61

Query Match 36.9%; Score 31; DB 11; Length 9;  
 Best Local Similarity 71.4%; Pred. No. 5.2e+05;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Y 7 WKQKDK 13  
 |:|:|:  
 b 2 WKKKKK 8

RESULT 6  
 US-10-108-844-5  
 Sequence 5, Application US/10108844  
 Publication No. US20030170894A1  
 GENERAL INFORMATION:  
 APPLICANT: Rice, Kevin G.  
 Wadhwa, Manpreet S.  
 TITLE OF INVENTION: Peptides for Gene Delivery  
 NUMBER OF SEQUENCES: 11  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: MEDLEN & CARROLL, LLP  
 STREET: 220 Montgomery Street, Suite 2200  
 CITY: San Francisco  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 94104  
 COMPUTER: READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC Compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATE:  
 APPLICATION NUMBER: US/10/108,844  
 FILING DATE: 28-Mar-2002

Protein - Protein search, using sw model

on: October 7, 2003, 16:34:43 ; Search time 102.059 Seconds  
 (without alignments)  
 539,670 Million cell updates/sec

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 perfect score: 1856  
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scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

number of hits satisfying chosen parameters: 1107863

DB seq length: 0  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query	Match	Length	DB	ID	Description
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2	1856	100.0	347	21	AAY33136		Human LFA3TRP transmembrane
3	1856	100.0	347	22	AAB61160		Human LFA3TRP fibroblast
4	1856	100.0	347	23	ABG70766		Human Lymphocyte LFA3TRP
5	1856	100.0	347	23	ABB81298		Human LFA3TRP protein
6	1856	100.0	347	23	AAT62298		LFA3/1 integrin fusion
7	1856	100.0	347	24	ABP58178		Murine LFA-3, M
8	1856	99.4	351	24	AAB281995		Human LFA-3/1 TIGG
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No is the number of results predicted by chance to have a derived. No is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

IMMORTALS

Result No.	Score	Query Match	Length	DB ID	Description
1	1856	100.0	347	13 AAR27163	CD2 binding LFA
2	1856	100.0	347	21 AAY8136	Human transmembrane
3	1856	100.0	347	22 AAB61160	Human LFA3/TPP fu
4	1856	100.0	347	23 ABG10766	Human Lymphocyte
5	1856	100.0	347	23 ABB81194	Human LFA3/TPP fu
6	1856	100.0	347	23 AAT6228	LFA3/TGG fusion
7	1856	100.0	347	24 ABP8178	Murine LFA-3
8	1845	99.4	351	23 ABB81195	Human LFA-3/TGG
9	1834	98.8	347	14 AAR34224	Amino acid sequence

omo sapiens.

tribution.

ey 25+ 20

### Description

卷之三

CD2 binding LFA-1

Human LFA3TIP f

## Human lymphocyte

Human LFA3TIP protein

LFA3/Lgg fusion Mu rine T-FA = 3

Human LEA-3/Tag

## Amino acid sequence

	key	Location	Qualifiers
PH	peptide	1..28	/label= LPA-3-signal
PT	region	29..120	/label= LPA-3_aminoacids_1..92
PT	region	121..130	/label= IgG1_hinge
PT	domain	131..239	/label= IgG1_CH2
PT	domain	240..347	/label= IgG1_CH3
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XX			16-SER1-1002
PN			

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minimum DB seq length: 0  
maximum DB seq length: 200000000  
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maximum Match 100%  
Listing first 45 summaries

Protein - protein search, using sw model  
 on: October 7, 2003, 16:34:43 ; Search time 102.059 Seconds  
 (without alignments)  
 539.670 Million cell updates/sec

Title: US-09-730-465-8  
 perfect score: 1856  
 sequence: 1 MVAGSDAGRAGLVLSVVCILL.....MHEALHNHYTQKSLISLSPGK 347

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

1107863 seqs , 158726573 residues  
 searched:

XX	12-MAR-1992;	92EP-0104320.	XX	LFA3; CD2; cell signalling; modulation; lymphocyte; T cell; KW memory effector T lymphocyte; psoriatic arthritis; KW rheumatoid arthritis; multiple sclerosis; atopic dermatitis; KW uveitis; inflammatory bowel disease; Crohn's disease; KW ulcerative colitis; cutaneous T cell lymphoma; inhibition; treatment; KW therapy.
XX	PA	(BIOJ ) BIOPHEN INC.	XX	XX
PI	Miller GT, Rosa MD, Wallner BP;	OS	OS	Homo sapiens.
XX	XX	XX	XX	WO20012113-A2.
DR	WP1; 1992-309760/38.	PN	PN	WPI; 2000-282926/24.
DR	N-PSDB; AAQ28634.	XX	XX	N-PSDB; AAZ33401.
XX	CD2-binding domain of lymphocyte function associated antigen-3 and DNA - for diagnosing and treating inflammation and auto-immune diseases, e.g. systemic lupus erythematosus and rheumatoid arthritis	PT	PT	09 MAR-2000.
PT	PT	PT	PT	31-AUG-1999;
PT	PT	PR	PR	99WO-US20026.
XX	XX	XX	XX	31-AUG-1998;
PS	Claim 13; Fig 12; 85pp; English.	PA	PA	98US-0098456.
XX	XX	XX	XX	(BIOJ ) BIOPHEN INC.
CC	The plasmid psAB152 contains the DNA sequence encoding the LFA-3 signal sequence, the amino terminal 92 amino acids of mature LFA-3, ten amino acids of the hinge region of IgG1 and the CH2 and CH3 constant domains of IgG1 (see AAQ28678-9 and AAQ28681-2 for details of the construction of psAB152). A NotI fragment containing the coding sequence of psAB152 was used in the construction of expression vector pMDR(92)ig-3 which can be stably maintained in CHO cells to bind to CD2 and inhibit T cell activation, making it useful to treat acute and chronic inflammation, autoimmune disease and in immunomodulation. (Updated on 25-MAR-2003 to correct PN field.)	CC	CC	Modulation of LFA3/CD2 interaction by administration of a CD2 binding agent inhibits CD2 signalling and T cell proliferation and activation and more particularly modulates the number and/or distribution of memory effector T lymphocytes. The method can be used for treating a condition in a subject where the condition is characterized by memory effector T lymphocytes playing a role in the pathogenesis of the condition such as psoriatic arthritis, rheumatoid arthritis, multiple sclerosis, atopic dermatitis, uveitis, inflammatory bowel disease, Crohn's disease, ulcerative colitis and cutaneous T cell lymphoma and where the method comprises administering to the subject an amount of CD2 binding agent sufficient to modulate the memory effector T lymphocytes. The methods provide inhibition of antigen specific interactions for all antigens present, inhibition of T cell activation, no general immunosuppression, and possibly induction of tolerance.
CC	Sequence 347 AA;	CC	CC	Modulation of LFA3/CD2 interaction by administration of a CD2 binding agent inhibits CD2 signalling and T cell proliferation and activation and more particularly modulates the number and/or distribution of memory effector T lymphocytes. The method can be used for treating a condition in a subject where the condition is characterized by memory effector T lymphocytes playing a role in the pathogenesis of the condition such as psoriatic arthritis, rheumatoid arthritis, multiple sclerosis, atopic dermatitis, uveitis, inflammatory bowel disease, Crohn's disease, ulcerative colitis and cutaneous T cell lymphoma and where the method comprises administering to the subject an amount of CD2 binding agent sufficient to modulate the memory effector T lymphocytes. The methods provide inhibition of antigen specific interactions for all antigens present, inhibition of T cell activation, no general immunosuppression, and possibly induction of tolerance.
XX	Query Match 100.0%; Score 1856; DB 13; Length 347; Best Local Similarity 100.0%; Pred. No. 1.7e-128; Mismatches 0; Matches 347; Conservative 0; Indels 0; Gaps 0;	XX	XX	Modulation of LFA3/CD2 interaction by administration of a CD2 binding agent inhibits CD2 signalling and T cell proliferation and activation and more particularly modulates the number and/or distribution of memory effector T lymphocytes. The method can be used for treating a condition in a subject where the condition is characterized by memory effector T lymphocytes playing a role in the pathogenesis of the condition such as psoriatic arthritis, rheumatoid arthritis, multiple sclerosis, atopic dermatitis, uveitis, inflammatory bowel disease, Crohn's disease, ulcerative colitis and cutaneous T cell lymphoma and where the method comprises administering to the subject an amount of CD2 binding agent sufficient to modulate the memory effector T lymphocytes. The methods provide inhibition of antigen specific interactions for all antigens present, inhibition of T cell activation, no general immunosuppression, and possibly induction of tolerance.
QY	1 MVAGSDAGRAIGVLSVCLLHCFCFISCFQQIYGVYGVNTPHVPNSNPLKEYLNKKK 60	QY	1 MVAGSDAGRAIGVLSVCLLHCFCFISCFQQIYGVYGVNTPHVPNSNPLKEYLNKKK 60	Query Match 100.0%; Score 1856; DB 21; Length 347; Best Local Similarity 100.0%; Pred. No. 1.7e-128; Mismatches 0; Indels 0; Gaps 0;
Db	1 MVAGSDAGRAIGVLSVCLLHCFCFISCFQQIYGVYGVNTPHVPNSNPLKEYLNKKK 60	Db	1 MVAGSDAGRAIGVLSVCLLHCFCFISCFQQIYGVYGVNTPHVPNSNPLKEYLNKKK 60	QY 1 DVAAELENSEFRAFSSFKNRYVLDIYSGSTIYTNTSSDEYMEESPNTIDMKFLYY 120
QY	61 DVAAELENSEFRAFSSFKNRYVLDIYSGSTIYTNTSSDEYMEESPNTIDMKFLYY 120	QY	61 DVAAELENSEFRAFSSFKNRYVLDIYSGSTIYTNTSSDEYMEESPNTIDMKFLYY 120	Db 61 DVAAELENSEFRAFSSFKNRYVLDIYSGSTIYTNTSSDEYMEESPNTIDMKFLYY 120
Db	61 DVAAELENSEFRAFSSFKNRYVLDIYSGSTIYTNTSSDEYMEESPNTIDMKFLYY 120	QY	121 DKTHTCPCPAPELLGGPSVLEPKPKDTLIMSRTEPEVKFNWYD 180	QY 121 DKTHTCPCPAPELLGGPSVLEPKPKDTLIMSRTEPEVKFNWYD 180
QY	121 DKTHTCPCPAPELLGGPSVLEPKPKDTLIMSRTEPEVKFNWYD 180	Db	121 DKTHTCPCPAPELLGGPSVLEPKPKDTLIMSRTEPEVKFNWYD 180	Db 121 DKTHTCPCPAPELLGGPSVLEPKPKDTLIMSRTEPEVKFNWYD 180
QY	181 GVEVHNAAKTRKTRREQINSTRVSVLTLVQDWNLNGKEYCKVSKNKAAPLERTISAK 240	QY	181 GVEVHNAAKTRKTRREQINSTRVSVLTLVQDWNLNGKEYCKVSKNKAAPLERTISAK 240	QY 1 DVAYELENSEFRAFSSFKNRYVLDIYSGSTIYTNTSSDEYMEESPNTIDMKFLYY 120
Db	181 GVEVHNAAKTRKTRREQINSTRVSVLTLVQDWNLNGKEYCKVSKNKAAPLERTISAK 240	Db	181 GVEVHNAAKTRKTRREQINSTRVSVLTLVQDWNLNGKEYCKVSKNKAAPLERTISAK 240	Db 181 GVEVHNAAKTRKTRREQINSTRVSVLTLVQDWNLNGKEYCKVSKNKAAPLERTISAK 240
QY	241 GQPREQVYTLPPSRDELTKNQSVLTCIYGFPSVSDIAVWEQSOPENNYKTPPVLD 300	QY	241 GQPREQVYTLPPSRDELTKNQSVLTCIYGFPSVSDIAVWEQSOPENNYKTPPVLD 300	QY 181 GVEVHNAAKTRKTRREQINSTRVSVLTLVQDWNLNGKEYCKVSKNKAAPLERTISAK 240
Db	241 GQPREQVYTLPPSRDELTKNQSVLTCIYGFPSVSDIAVWEQSOPENNYKTPPVLD 300	Db	241 GQPREQVYTLPPSRDELTKNQSVLTCIYGFPSVSDIAVWEQSOPENNYKTPPVLD 300	Db 181 GVEVHNAAKTRKTRREQINSTRVSVLTLVQDWNLNGKEYCKVSKNKAAPLERTISAK 240
QY	301 DGSFFFLYSKLVQDTSRSLRQOGNVSFCSCVMHEALHNHYTQKSLSLSPGK 347	QY	301 DGSFFFLYSKLVQDTSRSLRQOGNVSFCSCVMHEALHNHYTQKSLSLSPGK 347	QY 241 GQPREQVYTLPPSRDELTKNQSVLTCIYGFPSVSDIAVWEQSOPENNYKTPPVLD 300
Db	301 DGSFFFLYSKLVQDTSRSLRQOGNVSFCSCVMHEALHNHYTQKSLSLSPGK 347	Db	301 DGSFFFLYSKLVQDTSRSLRQOGNVSFCSCVMHEALHNHYTQKSLSLSPGK 347	Db 241 GQPREQVYTLPPSRDELTKNQSVLTCIYGFPSVSDIAVWEQSOPENNYKTPPVLD 300
RESULT 2	AAV83136	ID AAV83136	Standard; Protein; 347 AA.	XX 24-JUL-2000 (first entry)
AC	AAV83136;	XX	XX	Human transmembrane LFA-3/IgG fusion protein LFA3TIP.

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 7, 2003, 16:45:48 ; Search time 42.5245 Seconds  
(without alignments)  
784.736 Million cell updates/sec

Title: US-09-730-465-8

Perfect score: 1836

Sequence: 1 MVAGSDAGRAGLGVLSVYCLL.....MHEALHNHYTQKSLSLSPGK 347

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 9618682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR\_76:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	1233	66.4	255	4	S31866		Ig gamma-1 chain C
2	1233	66.4	330	1	GHHU		Ig gamma-1 chain C
3	1228.5	66.2	374	2	S69339		Ig heavy chain V r
4	1180	63.6	234	2	PT0207		Ig gamma chain C r
5	1146	61.7	377	2	A23511		Ig gamma-3 chain C
6	1145	61.7	326	1	G2HU		Ig gamma-2 chain C
7	1144	61.6	377	2	A60764		Ig gamma-3 chain C
8	1135	61.2	327	1	G4HU		Ig gamma-4 chain C
9	1121	60.4	289	1	G3HWI		Ig gamma-3 heavy C
10	926.5	49.9	323	1	GHRB		Ig gamma chain C r
11	913.5	49.2	328	2	I47160		Ig gamma 2b chain
12	909.5	49.0	328	2	I47159		Ig gamma 2a chain
13	906.5	48.8	277	2	I47162		Ig gamma 4 chain C
14	894.5	48.2	328	2	I47158		Ig gamma 1 chain C
15	892	48.1	329	1	G2GP		Ig gamma-2 chain C
16	886.5	47.8	328	2	I47161		Ig gamma 3 chain C
17	877.5	46.2	220	2	S22080		Ig heavy chain pre
18	846	45.6	308	2	C30554		Ig heavy chain C r
19	846	45.6	472	2	S31459		Ig gamma-1 chain C
20	845.5	45.6	329	1	G3MSC		Ig gamma-3 chain C
21	838	45.2	333	2	PS0018		Ig gamma-2b chain
22	834.5	45.0	398	1	G3MSM		Ig gamma-3 chain C
23	829.5	44.7	444	2	PC4436		monoclonal antibody
24	818.9	44.1	326	2	PS0017		Ig gamma-1 chain C
25	818.5	44.1	324	1	G1MS		Ig gamma-1 chain C
26	813.5	43.8	393	1	G1MSM		Ig gamma-1 chain C
27	812	43.8	329	2	S00847		Ig gamma-2c chain
28	811.5	43.7	330	1	G2MSA		Ig gamma-2a chain
29	811.5	43.7	469	2	S37483		Ig gamma-2a chain

#### RESULT 1

S31866

Ig gamma-1 chain C region - synthetic

C;Species: synthetic

A;Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli

C;Date: 06-Jan-1995 #sequence\_revision 17-Mar-1997 #text\_change 19-May-2000

C;Accession: S31866

R;Filipula, D.

submitted to the EMBL Data Library, February 1993

A;Description: Screening method for protein-protein interactions of cloned gene pro-

A;Reference number: S31866

A;Accession: S31866

A;Molecule type: mRNA

A;Residues: 1-245 <PFL>

A;Cross-references: EMBL:X70421; NID:q33068; PIDN:CAA49866-1; PID:g33069

C;Keywords: immunoglobulin outer membrane protein A precursor

F;1-22/Region: Escherichia coli outer membrane protein A precursor

F;2-3-25/Region: human Ig gamma-1 chain C region

Query Match 66.4%; Score 1233; DB 4; Length 255;

Best Local Similarity 100.0%; Pred. No. 1.5e-80; Mismatches 0; Indels 0; Gaps 0;

QY 121 DKTHTCPPCPAPEELLGGPSVFLPPPKDITMISRTPETVYVVDYSHEDPEVKFNWYD 180

Db 29 DTHTCPCPAPEELLGGPSVFLPPPKDITMISRTPETVYVVDYSHEDPEVKFNWYD 88

QY 181 GVEVHNKTKPKEEQYNTSYRVTYVSVTLYHQDWLNGKEYCKVYSNKLAPAPIEKTSKAK 240

Db 89 GVEVHNKTKPKEEQYNTSYRVTYVSVTLYHQDWLNGKEYCKVYSNKLAPAPIEKTSKAK 148

QY 241 GPREPQYVTPPSRDELTKQVSITLCLVKGFPYPSDIAVEMESNGOPENNYKTTPPVLD 300

Db 149 GPREPQYVTPPSRDELTKQVSITLCLVKGFPYPSDIAVEMESNGOPENNYKTTPPVLD 208

QY 301 DGSFFLYSKLTVDKSRM0QGNVFSCTYMEALHNHTQKSLSLSPK 347

Db 209 DGSFFLYSKLTVDKSRM0QGNVFSCTYMEALHNHTQKSLSLSPK 255

#### RESULT 2

GHU

Ig gamma-1 chain C region - human

C;Species: Homo sapiens (man)

C;Date: 31-Jan-1981 #sequence\_revision 18-Aug-1982 #text\_change 16-Jul-1999

C;Accession: A93433; S33861; S33871; B90563; A91723; A02146

R;Ellison, J.W.; Berson, B.J.; Hood, L.E.

Nucleic Acids Res. 10, 4071-4079, 1982

A;Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.

A;Reference number: A93433; M01D:6287432; PMID:6287432

A;Accession: A93433

A;Molecule type: DNA

A;Residues: 1-330 <ELL>	A;Cross-references: EMBL:217370	A;Note: this sequence has the Glm(17) allotypic marker, 97-Lys, and the Glm(1) markers, submitted to the EMBL Data Library, October 1992	A;Reference number: S33904	A;Accession: S36861	A;Molecule type: DNA	A;Residues: 2-310 <HAR>	A;Cross-references: EMBL:217370	A;Residues: 88-113;235-330 <TAK>	A;Cross-references: EMBL:217310	A;Title: Structure of human immunoglobulin gamma genes: implications for evolution of a gamma chain. <i>Biochemistry</i> 9, 671-679, 1982	A;Reference number: S33887	A;Accession: S33887	A;Residues: 88-113;235-330 <TAK>	A;Cross-references: EMBL:217310	A;Title: The covalent structure of a human gamma-g immunoglobulin. VII. Amino acid sequence. <i>Biochemistry</i> 9, 3161-3170, 1970	A;Reference number: A90563	A;Accession: B90563	A;Molecule type: Protein	A;Residues: 1-96;R',98-135 <QUN>	A;Note: this sequence has the Glm(3) marker, 97-Arg	A;Contents: myeloma protein Eu	A;Accession: A90564;	A;Reference number: A90564;	A;Contents: myeloma protein	A;Accession: B91668	A;Molecule type: Protein	A;Residues: 136-154;Q',156-165;Q',167-176;Q',178-194;N',196-197;D',199-238;E',240;R';Schmidt, W.E.;Hilschmann, N.	A;Note: this sequence has the Glm(17) and Glm(1) markers	R;Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976	A;Title: Die Primärstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie), A;Reference number: A91668;	A;Accession: A91723;	A;Reference number: A91723;	A;Contents: annotation: disulfide bonds	A;Accession: A91723	A;Molecule type: Protein	A;Residues: 98-115;K',98-96;Q',36-96;Q',117-197;D',199-238;D',240;L',242-268;E',27;R';Schmidt, W.E.;Jung, H.D.;Palm, W.;Hilschmann, N.	A;Note: this sequence has the Glm(17) and Glm(1) markers	R;Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983	A;Title: Die Primärstruktur des kristallisierten monoklonalen Immunglobulins IgG1 KOI, A;Reference number: A91723;	A;Accession: A91723	A;Reference number: A91723	A;Contents: annotation: disulfide bonds	A;Accession: A91723	A;Molecule type: Protein	A;Residues: 96-R',98-197;D',199-238;E',240;M',242-266;D',268-271;D',273-330 <SCHE>	A;Note: this sequence has the Glm(3) and Glm(non-1) markers	R;Gall, W.E.;Edelman, G.M.	Biochemistry 9, 3188-3196, 1970	A;Title: The covalent structure of a human gamma-g immunoglobulin. X. Intrachain disulfide embond cleavage products, and the disulfide bridges.	R;Dreker, L.;Schwarz, J.;Reichel, W.;Hilschmann, N.	A;Reference number: A91667;MUID:77070267;	A;Accession: A91667	A;Genetics: GDB:IGRGL1	A;Cross-references: GDB:120085; OMIM:147100	A;Map Position: 14q32.33-14q32.33	A;Introns: 99/1; 114/1; 22/1	C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kar-		
Query Match 66.4%; Score 1233; DB 1; Length 330;	Best Local Similarity 100.0%; Pred. No. 2.1e-10;	Indels 0; Gaps 0;	Matches 227; Conservative 0; Mismatches 0;	QY	121 DKTHTCPPCPAPELLGGPSVFLPPPKDLMISRTPEVTCVVDYSHEDPEPKFENWVD 180	Db	104 DKHTCPCPAPELLGGPSVFLPPPKDLMISRTPEVTCVVDYSHEDPEPKFENWVD 163	QY	181 GVEYHNATKPKPREQYNTYRVSYSLTVLHQDVLNGKEYKCKVSNKALPATEKTIASK 240	Db	164 GVEYHNATKPKPREQYNTYRVSYSLTVLHQDVLNGKEYKCKVSNKALPATEKTIASK 223	QY	241 GQREPQVYTLPPSRDELTKNOVSLTCLVKGKFYPSDIAVEWSNGOPENNKKTPPYLDS 300	Db	224 GQREPQVYTLPPSRDELTKNOVSLTCLVKGKFYPSDIAVEWSNGOPENNKKTPPYLDS 283	QY	301 DGSPFLYSKLTVDKSRWQOGNPFSCSVYHEALENHYTKSLSLSPGK 347	Db	284 DGSPFLYSKLTVDKSRWQOGNPFSCSVYHEALENHYTKSLSLSPGK 330	RESIDUE 3	S69339	IG heavy chain V region precursor - human	C;Species: Homo sapiens (man)	C;Date: 19-Mar-1997; #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000	R;Khamlich, S.;S72664	Eur. J. Biochem. 229, 54-60, 1995	A;Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease	A;Reference number: S69339; MUID:95262687; PMID:7744049	A;Accession: S69339	A;Status: preliminary	A;Molecule type: mRNA	A;Residues: 1-374 <KHA>	A;Cross-references: EMBL:X81695	R;Khamlich, A.A.	Submitted to the EMBL Data Library, September 1994	A;Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease	A;Reference number: S69339; MUID:95262687; PMID:7744049	A;Accession: S69339	A;Status: preliminary	A;Molecule type: mRNA	A;Residues: 1-140, C',142-374 <KH2>	A;Cross-references: EMBL:X81695	C;Superfamily: immunoglobulin C region; immunoglobulin homology	Query Match 66.2%; Score 1228.5%; DB 2; Length 374;	Best Local Similarity 79.3%; Pred. No. 5.2e-80;	Indels 29; Gaps 1;	Matches 234; Conservative 10; Mismatches 22;	QY	82 YLDTYSGSLIYNTSSDEDEYEMESPNTDTMKFFL-----	Db	80 YSPSLRTRLITKOTSKNOVLMINTYDPAITANYYCYSVEYQGYRFHNSQGFLYT 139	QY	119 -----YVDKTHTCPPCPAPELLGGPSVFLPPPKDLMISRTPEVTCVVDYSHEDPE 172	Db	140 VSSEPKSCDKHTCPCPAPELLGGPSVFLPPPKDLMISRTPEVTCVVDYSHEDPE 199	QY	173 VKFNNYVDGYEVHNATKPKPREQYNTYRVSYSLTVLHQDVLNGKEYKCKVSNKALPAPI 232	Db	200 VKFNNYVDGYEVHNATKPKPREQYNTYRVSYSLTVLHQDVLNGKEYKCKVSNKALPAPI 259

Result No.	Score	Query	Match	Length	DB ID	Description
1	1233	66.4	330	1	GC1_HUMAN	P01857 homo sapien
2	1145.5	61.7	326	1	GC2_HUMAN	P01859 homo sapien
3	1135	61.2	327	1	GC4_HUMAN	P01861 homo sapien
4	1126	60.7	290	1	GC3_HUMAN	P01860 homo sapien
5	926.5	49.9	323	1	GC_RABIT	P01870 oryctolagus cuniculus
6	892	48.1	329	1	GC2_CAVPO	P01862 cavia porcellus
7	845.5	45.6	329	1	GC3_MOUSE	P02436 mus musculus
8	838	45.2	333	1	GCB_RAT	P20761 rattus norvegicus
9	834.9	45.0	398	1	GC3_MOUSE	P03987 mus musculus
10	819	44.1	326	1	GC1_RAT	P20759 rattus norvegicus
11	818.5	44.1	324	1	GC1_MOUSE	P01868 mus musculus
12	813.5	43.8	329	1	GC1_MOUSE	P01869 mus musculus
13	812	43.8	329	1	GCC_RAT	P20762 rattus norvegicus
14	811.5	43.7	330	1	GCA_MOUSE	P01863 mus musculus
15	806.5	44.5	339	1	GCAB_MOUSE	P01865 mus musculus
16	804	43.3	335	1	GCAB_MOUSE	P01864 mus musculus
17	787.5	42.4	322	1	GCA_RAT	P20760 rattus norvegicus
18	783.5	42.2	336	1	GCB_MOUSE	P01866 mus musculus
19	778.5	41.9	405	1	GCB_MOUSE	P01867 mus musculus
20	630	33.9	250	1	LFA3_HUMAN	P19456 homo sapien
21	368	19.8	421	1	EPC_RAT	P06336 mus musculus
22	366.5	19.7	429	1	EPC_RAT	P01855 rattus norvegicus
23	360.5	19.4	428	1	EPC_HUMAN	P01854 homo sapien
24	358.5	19.3	454	1	MDC_HUMAN	P01871 homo sapien
25	357	19.2	455	1	MDC_MOUSE	P01872 mus musculus
26	356.5	19.2	391	1	MUCB_HUMAN	P04420 homo sapien
27	351	18.9	458	1	MUCB_RABBIT	P03988 oryctolagus cuniculus
28	347	18.7	476	1	MUCM_MOUSE	P01873 mus musculus
29	342	18.4	479	1	MUCM_RABBIT	P04221 oryctolagus cuniculus
30	335	18.0	457	1	MUC_SUNMU	P20768 sunicus murinus
31	332	17.9	450	1	MDC_CANFA	P01874 canis familiaris
32	332	17.9	454	1	MUC_MESAU	P06337 mesocricetus auratus
33	302.5	16.3	438	1	HVC2_HETFR	P23085 heterodontus francisci

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41:\*

Scoring table: BLOSUM62

Perfect score: 1856

Sequence: 1 MVAGSDAGRALGVLSVYCLL.....MHEALHNHTQKSLSLSPSK 347

## ALIGNMENTS

RESULT 1  
GC1\_HUMAN  
ID : GCL\_HUMAN  
STANDARD;  
PRT; 330 AA.  
AC P01857;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE 19 gamma-1 chain C region.  
GN IGHG1.  
HO: Homo sapiens (Human).  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OC NCBI\_TaxID:9606;  
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OM protein - protein search, using sw model

Run on: October 7, 2003, 16:35:28 ; Search time 22.9632 seconds  
(without alignments)  
710.626 Million cells/sec

Title: US-09-730-465-8

Perfect score: 1856

Sequence: 1 MVAGSDAGRALGVLSVYCLL.....MHEALHNHTQKSLSLSPSK 347

SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).  
Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,  
Waxdal M.J., Edelman G.M.;  
"The covalent structure of a human gamma G-immunoglobulin. VII. Amino acid sequence of heavy-chain cyanogen bromide fragments H5-H7."  
[3]

SEQUENCE OF 136-129 (EU).  
Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,

RT	Intrachain disulfide bonds.";				
RL	Biotechnology 9:3188-3196(1970).				
RL	[7]				
RP	DISULFIDE BONDS.				
RX	Medline=770267; PubMed=1002129;				
RA	Dreker L., Schwarz J., Reichel W., Hilschmann N.;				
RA	"Rule of antibody structure. The primary structure of a monoclonal				
RT	IgG1 immunoglobulin (myeloma protein) I: Purification and				
RT	characterization of the protein, the L- and H-chains, the				
RT	cyanogen bromide cleavage products, and the disulfide bridges.";				
RT	Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).				
RN	[8]				
RP	X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).				
RX	Medline=81208100; PubMed=7236608;				
RA	Deisenhofer J.;				
RT	"Crystallographic refinement and atomic models of a human Fc fragment				
RT	and its complex with fragment B of protein A from <i>Staphylococcus</i>				
RT	aureus at 2.9- and 2.8-A resolution.";				
RL	Biotechnology 20:2363-2370(1981).				
CC	-1- MISCELLANEOUS: NIE HAS THE GLM(17) ALLOTPIC MARKER, 97-K, & THE				
CC	GLM(1) MARKERS, 239-D & 241-L. KOL & EU SEQUENCES HAVE THE GLM(3)				
CC	MARKER & THE GLM (NON-1) MARKERS.				
CC	-1- MISCELLANEOUS: NIE ALSO DIFFERS IN THE AMIDATION STATES OF				
CC	35,116,198,269 & 272.				
CC	-1- MISCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES				
CC	155, 166, 177, 195, 198, 269, AND 272 AND IN THE ORDER OF RESIDUES				
CC	268-272.				
CC	-1- MISCELLANEOUS: KOL ALSO DIFFERS IN THE AMIDATION STATES OF				
CC	RESIDUES 198,267&272.				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
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CC	use by non-profit institutions as long as its content is in no way				
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CC	-----				
DR	EMBL; J00288; AAC82527.1; ALT_INIT.				
DR	PTR; A93433; GHGU.				
DR	PDB; 1FC1; 15-JUL-92.				
DR	PDB; 1FC2; 15-JUL-92.				
DR	PDB; 1AJ7; 12-NOV-97.				
DR	PDB; 1D5B; 09-FEB-00.				
DR	PDB; 1D5I; 09-FEB-00.				
DR	PDB; 1D6V; 04-OCT-00.				
DR	PDB; 1DN2; 17-MAY-00.				
DR	PDB; 1E4K; 06-JUN-01.				
DR	PDB; 1FCC; 10-APR-02.				
DR	PDB; 1HZH; 12-JUN-02.				
DR	PDB; 1I7Z; 08-AUG-01.				
DR	PDB; 1IIS; 16-MAY-01.				
DR	PDB; 1IIX; 16-MAY-01.				
DR	PDB; 1L6X; 10-APR-02.				
DR	PDB; 2RCS; 12-NOV-97.				
DR	Genew; HGNC:5525; ICHG1.				
DR	MM: 147100; -				
DR	GC: 90-00056-24; C:membrane fraction; NAS.				
DR	GO: 60-00038-23; F:antigen binding activity; TAS.				
DR	GO: 60-0006955; P:immune response; NAS.				
DR	InterPro; IPR007110; Ig-like.				
DR	InterPro; IPR003597; Ig-cl.				
DR	InterPro; IPR003006; Ig_MHC.				
DR	Pfam; PF00047; Ig.				
DR	SMART; SM00407; IgCl.				
DR	PROSITE; PS00835; Ig_LIKE; 3.				
DR	PROSITE; PS00290; Ig_MHC; 2.				
KW	Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;				
KW	3D-structure.				
FT	NON_TER	1	1		
FT	DOMAIN	1	98		
FT	DOMAIN	99	110	CH1. HINGE.	
FT	DOMAIN	111	223	CH2.	
RESULT	2				
GC2_HUMAN					
ID	GC2_HUMAN				
STANDARD					
PRT;	326 AA.				

GenCore version 5.1.6  
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Om protein - protein search, using sw model

Run on: October 7, 2003, 16:45:18 ; Search time 102.909 Seconds  
(without alignments)  
870.128 Million cell updates/sec

Title: US-09-730-465-8

Perfect score: 1856

Sequence: 1 MYAGSDIGRALGVLSVYCL.....MHRALHNHYTQKSLISLSPGK 347

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL\_233:  
 1: sp\_archaea:  
 2: sp\_bacteria:  
 3: sp\_fungi:  
 4: sp\_human:  
 5: sp\_invertebrate:  
 6: sp\_mammal:  
 7: sp\_mhc:  
 8: sp\_organelle:  
 9: sp\_phage:  
 10: sp\_plant:  
 11: sp\_rabbit:  
 12: sp\_virus:  
 13: sp\_vertebrate:  
 14: sp\_unclassified:  
 15: sp\_virus:  
 16: sp\_bacterioplasmid:  
 17: sp\_archeap:  
 18: sp\_bacteria:  
 19: sp\_fungi:  
 20: sp\_human:  
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 22: sp\_mammal:  
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 841: sp\_virus:  
 842: sp\_bacterioplasmid:  
 843: sp\_bacteria:  
 844: sp\_fungi:  
 845: sp\_human:  
 846: sp\_invertebrate:  
 847: sp\_mammal:  
 848: sp\_mhc:  
 849: sp\_organelle:  
 850: sp\_phage:  
 851: sp\_plant:  
 852: sp\_rabbit:  
 853: sp\_virus:  
 854: sp\_vertebrate:  
 855: sp\_unclassified:  
 856: sp\_virus:  
 857: sp\_bacterioplasmid:  
 858: sp\_bacteria:  
 859: sp\_fungi:  
 860: sp\_human:  
 861: sp\_invertebrate:  
 862: sp\_mammal:  
 863: sp\_mhc:  
 864: sp\_organelle:  
 865: sp\_phage:  
 866: sp\_plant:  
 867: sp\_rabbit:  
 868: sp\_virus:  
 869: sp\_vertebrate:  
 870: sp\_unclassified:  
 871: sp\_virus:  
 872: sp\_bacterioplasmid:  
 873: sp\_bacteria:  
 874: sp\_fungi:  
 875: sp\_human:  
 876: sp\_invertebrate:  
 877: sp\_mammal:  
 878: sp\_mhc:  
 879: sp\_organel

RESULT 2		RESULT 3	
241	QGPREFQVYTLPPSDELTKNQVSITCLVKGFYPSDIAVEWSNQOPENNYKTPVLDLS 300   365 QGPREFQVYTLPPSDELTKNQVSITCLVKGFYPSDIAVEWSNQOPENNYKTPVLDLS 424 		
301	DGSFELYSKLVYDVKSRQGNVSCSYMHAEALHNHYTOKSLSLSGK 347   425 DGSFELYSKLVYDVKSRQGNVSCSYMHAEALHNHYTOKSLSLSGK 471 		
Y	Q96PQ8 PRELIMINARY; PRT: 701 AA. O96PQ8; 19; Created. AC 01-DEC-2001 (TRIMBrel. 19, Last sequence update) DT 01-DEC-2001 (TRIMBrel. 19, Last annotation update) DT 01-MAR-2003 (TRIMBrel. 23, Last annotation update) DE Factor VII active site mutant immunocoujugate. Homo sapiens (Human). JS Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Primates; Catarrhini; Hominoidea; Homo. NCBI_TAXID:9606; LN [1] XX		
Db	SEQUENCE FROM N.A. MEDLINE=21477448; PubMed=11595034; Hs2 Hu Z.; Garen A.; "targeting tissue factor on tumor vascular endothelial cells and tumor cells for immunotherapy in mouse models of prostatic cancer."; proc. Natl. Acad. Sci. U.S.A. 98:12180-12185 (2001). -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. EMBL: AF27274; AAC56661.; -. HSSP: P00761; IANL. InterPro: IPR000152; ASX_hydroxyl. InterPro: IPR00314; Chymotrypsin. InterPro: IPR000742; EGF_2. InterPro: IPR001881; EGF_Ca. InterPro: IPR001138; EGF-II. InterPro: IPR005209; EGF-like. InterPro: IPR002383; GLA_blood. InterPro: IPR007110; Ig-like. InterPro: IPR003597; Ig_C1. InterPro: IPR003006; Ig_MHC. InterPro: IPR001254; Ser_protease_Try. InterPro: IPR000294; VitK_dep_GLA. Pfam: PF00008; EGF; 2. Pfam: PF00008; Ig; 2. Pfam: PF00534; IgA; 1. Pfam: PF00089; trypsin; 1. Pfam: PF00047; Ig; 2. Pfam: PF00089; trypsin; 1. PRINTS: PRO0722; CHYNOTRYPSIN. PRINTS: PRO00010; EGF_BLOOD. PRINTS: PRO00001; GLABLOOD. SMART: SM00179; EGF_Ca; 1. SMART: SM00069; GLA; 1. SMART: SM00407; IgC1; 1. SMART: SM00020; TRYPSIN; 1. PROSITE: PS00010; ASX_HYDROXYL; 1. PROSITE: PS00020; GLABLOOD. PROSITE: PS00022; EGF_1.; 1. PROSITE: PS01186; EGF_2.; 1. PROSITE: PS01187; EGF_Ca; 1. PROSITE: PS00011; GLU_CARBOXYLATION; 1. PROSITE: PS50835; Ig_LIKE; 2. PROSITE: PS00290; Ig_MHC; 1. PROSITE: PS500240; TRYPSIN_DOM; 1. PROSITE: PS00134; TRYPSIN_HIS; 1. PROSITE: PS00135; TRYPSIN_SER; 1. Egg_Like domain; Hydrolase; Protease; Serine protease. SEQUENCE 701 AA; 77826 MW; 94AC6CEB42C992F CRC64; SQ	Query Match 66.4%; Score 1233; DB 4; Length 701; Best Local Similarity 100.0%; Pred. No. 2.9e-100; Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0 121 DKTTCPCPQAPPTGGPSVFLPPPKPDKTMTSRTPVCVYDVSHEDPVKENWYD 180	0

RESULT 3									
Db	475	DKTICPPCPAPELIGGSPSYFLPPKPKDITLISRTPEYTCVYDVSHEDPEVKENYVD	534						
Qy	181	GVEVHAKTKPREEQNSTERVVSYLTVLHQDWLNGKEYCKVSKNALPAPIEKTKSKAK	240						
Db	535	GVEVHAKTKPREEQNSTERVVSYLTVLHQDWLNGKEYCKVSKNALPAPIEKTKSKAK	594						
Qy	241	GQPREQVTLLPSPRDELTKNOVSLLTCLYGFPSDIAVEWSNGOPENNYKTPPPVLD	300						
Db	595	GQPREQVTLLPSPRDELTKNOVSLLTCLYGFPSDIAVEWSNGOPENNYKTPPPVLD	654						
Qy	301	DGSFFLYSKLTVDKSRWQGNVFSCSYMHALHNHYTQKSLSLSPGK	347						
Db	655	DGSFFLYSKLTVDKSRWQGNVFSCSYMHALHNHYTQKSLSLSPGK	701						
RESULT 4									
Qy	08NA419	PRELIMINARY;	PRT;	521 AA.					
AC	Q8NA419;								
DT	01-OCT-2002	(TREMBLrel.	22;	Created)					
DR	01-OCT-2002	(TREMBLrel.	22;	Last sequence update)					
DT	01-NAPR-2003	(TREMBLrel.	23;	Last annotation update)					
DE	Hypothetical protein.								
OS	Homo sapiens (Human).								
OS	Karyota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostonii;								
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.								
NCBI_TAXID	9606;								
RN	[1]								
RP	SEQUENCE FROM N.A.								
RC	TISSUE=Primary B-Cells from Tonsils;								
RA	Staatsberg R.;								
RL	Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.								
DR	BC03178; AAH3178.1;	-.							
DR	InterPro; IPR007110; Ig-like.								
DR	InterPro; IPR003597; Ig_c1.								
DR	InterPro; IPR003006; Ig_MHC.								
DR	InterPro; IPR003596; Ig_v.								
DR	Pfam0047; ig; 4.								
DR	SMART; SM00407; IgCl_3.								
DR	SMART; SM00406; IgV_1.								
DR	PROSITE; PS50835; Ig_LIKE; 4.								
DR	PROSITE; PS00230; Ig_MHC; 2.								
KW	Hypothetical protein.								
SQ	SEQUENCE 521 AA; 57156 MW;	2ACTD22E72D6CAA2	CRC64;						
Query Match	61.5%	Score 1142;	DB 4;	Length 521;					
Best Local Similarity	92.1%	Pred No. 2.	2e-92;						
Matches	209;	Conservative	9;	M:smatches 9;	Indels 0;	Gaps 0			
Qy	121	DKTHICPPCPAPELIGGSPSYFLPPKPKDITMISRTPEYTCVYDVSHEDPEVKENYVD	184						
Db	295	DTPPPCPRCPAPELIGGSPSYFLPPKPKDITMISRTPEYTCVYDVSHEDPEVKENYVD	355						
Qy	181	GVEVHAKTKPREEQNSTERVVSYLTVLHQDWLNGKEYCKVSKNALPAPIEKTKSKAK	24						
Db	355	GVEVHAKTKPREEQNSTERVVSYLTVLHQDWLNGKEYCKVSKNALPAPIEKTKSKAK	414						
Qy	241	GQPREQVTLLPSPRDELTKNOVSLLTCLYGFPSDIAVEWSNGOPENNYKTPPPVLD	300						
Db	415	GQPREQVTLLPSPRDELTKNOVSLLTCLYGFPSDIAVEWSNGOPENNYKTPPPVLD	474						
Qy	301	DGSFFLYSKLTVDKSRWQGNVFSCSYMHALHNHYTQKSLSLSPGK	347						
Db	475	DGSFFLYSKLTVDKSRWQGNVFSCSYMHALHNHYTQKSLSLSPGK	521						

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 7, 2003, 16:47:23 ; Search time 34.8701 Seconds  
(without alignments) 421.045 Million cell updates/sec

Title: US-09-730-465-8  
Perfect score: 1856  
Sequence: 1 MVAGSDAGRALGVLSVYVCLL.....MHEALHNHYTQKSLSLSPGK 347

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328117 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717.

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_2A:\*

1: /cgn2\_6\_ptodata/1/iaa/5A\_COMB.pep:\*

2: /cgn2\_6\_ptodata/1/iaa/5B\_COMB.pep:\*

3: /cgn2\_6\_ptodata/1/iaa/6A\_COMB.pep:\*

4: /cgn2\_6\_ptodata/1/iaa/6B\_COMB.pep:\*

5: /cgn2\_6\_ptodata/1/iaa/PCUTS\_COMB.pep:\*

6: /cgn2\_6\_ptodata/1/iaa/backdata1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	1856	100.0	347	1	US-07-940-861-43	Sequence 43, Appl.
2	1856	100.0	347	1	US-08-459-512-43	Sequence 43, Appl.
3	1856	100.0	347	2	US-08-459-657-43	Sequence 43, Appl.
4	1856	100.0	347	2	US-08-460-132-43	Sequence 43, Appl.
5	1856	100.0	347	3	US-08-466-465-8	Sequence 8, Appl.
6	1856	100.0	347	5	PCT-US92-100-43	Sequence 43, Appl.
7	1249	67.3	859	4	US-09-313-942-7	Sequence 7, Appl.
8	1249	67.3	1158	4	US-09-313-942-26	Sequence 26, Appl.
9	1249	67.3	1168	4	US-09-313-942-24	Sequence 24, Appl.
10	1247	67.2	446	4	US-09-157-4523-12	Sequence 12, Appl.
11	1242	66.9	388	3	US-09-131-247-16	Sequence 16, Appl.
12	1239.5	66.8	482	4	US-09-189-129-2	Sequence 2, Appl.
13	1239	66.8	442	5	PCT-US96-1004-3-9	Sequence 9, Appl.
14	1239	66.8	704	4	US-09-590-656-2	Sequence 2, Appl.
15	1239	66.8	704	4	US-09-713-764-2	Sequence 2, Appl.
16	1238.5	66.7	424	5	PCT-US95-03866-12	Sequence 12, Appl.
17	1238.5	66.7	424	5	PCT-US95-03866-14	Sequence 14, Appl.
18	1238.5	66.7	437	5	PCT-US96-1004-3-11	Sequence 11, Appl.
19	1238.5	66.7	691	4	US-09-313-942-20	Sequence 20, Appl.
20	1238.5	66.7	694	4	US-09-313-942-22	Sequence 22, Appl.
21	1238	66.7	680	3	US-08-227-496C-15	Sequence 15, Appl.
22	1237	66.6	229	4	US-09-122-444-2	Sequence 2, Appl.
23	1236	66.6	592	4	US-09-313-942-8	Sequence 8, Appl.
24	1235.5	66.6	488	3	US-08-776-111-2	Sequence 2, Appl.
25	1234	66.5	552	1	US-08-243-010-6	Sequence 6, Appl.
26	1233.5	66.5	994	4	US-09-313-942-18	Sequence 18, Appl.
27	1233.5	66.5	994	4	US-09-313-942-32	Sequence 32, Appl.

#### ALIGNMENTS

RESULT 1  
US-07-940-861-43  
; Sequence 43, Application US/07940861  
; Patent No. 5547853

GENERAL INFORMATION:  
APPLICANT: BIOCERN, INC.  
APPLICANT: WALLNER, Barbara P.  
APPLICANT: MILLER, Glenn T.  
APPLICANT: ROSA, Margaret D.  
TITLE OF INVENTION: CD2-BINDING DOMAIN OF LYMPHOCYTE  
TITLE OF INVENTION: FUNCTION ASSOCIATED ANTIGEN 3  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Neave  
STREET: 875 Third Avenue  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10022-6250

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patientin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/940,861  
FILING DATE: 21-OCT-1992  
CLASSIFICATION: 514

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/02050  
FILING DATE: 12-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/667,971  
FILING DATE: 12-MAR-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/770,967  
FILING DATE: 07-OCT-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: HALEY, James F., Jr.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: B151C1P2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)715-0600  
TELEFAX: (212)715-0673  
TELEFAX: 14-8367  
INFORMATION FOR SEQ ID NO: 43:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 347 amino acids  
TYPE: amino acid  
TOPOLOGY: linear

MOLECULE TYPE: protein

JS-07-940-061-43

Query Match 100.0%; Score 1856; DB 1; Length 347;  
Best Local Similarity 100.0%; Pred. No. 4.1e-163;  
Matches 347; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 MYAGSDAGRALGAVLSQLVCLLRCGFISCFSQIYGVYGNVTPHYPNSVPLKEYLWKKQK 60  
Db 1 MYAGSDAGRALGAVLSQLVCLLRCGFISCFSQIYGVYGNVTPHYPNSVPLKEYLWKKQK 60

Qy 61 DKVAALENSEFRASSFKNRYLDTVSGSLITYNLSSDEYEVESPNTDTMKFFLY 120  
Db 61 DKVAALENSEFRASSFKNRYLDTVSGSLITYNLSSDEYEVESPNTDTMKFFLY 120

Qy 121 DKHTCPCPAPDELLGGPSVLFPPKPKDTMISRPEVTCVVDYDSEDPEVKENWYD 180  
Db 121 DKHTCPCPAPDELLGGPSVLFPPKPKDTMISRPEVTCVVDYDSEDPEVKENWYD 180

Qy 181 GQEVHNAAKTKPREEQNTSYRVSVTILHODWLNGKEYKCKVSNKALPAPETISKAK 240  
Db 181 GQEVHNAAKTKPREEQNTSYRVSVTILHODWLNGKEYKCKVSNKALPAPETISKAK 240

Qy 241 GQPREQVYTLPSRDELTKNQVSLTCLVKGFPSDIAVEWNSQOPENNYKTPPVLD 300  
Db 241 GQPREQVYTLPSRDELTKNQVSLTCLVKGFPSDIAVEWNSQOPENNYKTPPVLD 300

Qy 301 DGSEFFLKSQTLVTDKSRSQGNVFTCSVYHEALHNHYTQKSLSLSGK 347  
Db 301 DGSEFFLKSQTLVTDKSRSQGNVFTCSVYHEALHNHYTQKSLSLSGK 347

RESULT 2

US-08-459-512-43  
; Sequence 43, Application US/08459512  
; Patent No. 5726677  
; TITLE OF INVENTION: CD2-B-BINDING DOMAIN OF LYMPHOCYTE  
; NUMBER OF SEQUENCES: 43  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Fish & Neave  
; STREET: 875 Third Avenue  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10022-6250  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/459,512  
; FILING DATE: 02-JUN-1995  
; CLASSIFICATION: 514  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US92/02050  
; FILING DATE: 12-MAR-1992  
; APPLICATION NUMBER: US 07/667,971  
; FILING DATE: 07-OCT-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: HALEY, James F., Jr.  
; REGISTRATION NUMBER: 27,794  
; REFERENCE/DOCKET NUMBER: B15C1P2  
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)715-0600  
TELEFAX: (212)715-0673  
TELEX: 14-8367  
; INFORMATION FOR SEQ ID NO: 43:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 347 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-459-512-43

Query Match 100.0%; Score 1856; DB 1; Length 347;  
Best Local Similarity 100.0%; Pred. No. 4.1e-163;  
Matches 347; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 MYAGSDAGRALGAVLSQLVCLLRCGFISCFSQIYGVYGNVTPHYPNSVPLKEYLWKKQK 60  
Db 1 MYAGSDAGRALGAVLSQLVCLLRCGFISCFSQIYGVYGNVTPHYPNSVPLKEYLWKKQK 60

Qy 61 DKVAALENSEFRASSFKNRYLDTVSGSLITYNLSSDEYEVESPNTDTMKFFLY 120  
Db 61 DKVAALENSEFRASSFKNRYLDTVSGSLITYNLSSDEYEVESPNTDTMKFFLY 120

Qy 121 DKHTCPCPAPDELLGGPSVLFPPKPKDTMISRPEVTCVVDYDSEDPEVKENWYD 180  
Db 121 DKHTCPCPAPDELLGGPSVLFPPKPKDTMISRPEVTCVVDYDSEDPEVKENWYD 180

Qy 181 GQEVHNAAKTKPREEQNTSYRVSVTILHODWLNGKEYKCKVSNKALPAPETISKAK 240  
Db 181 GQEVHNAAKTKPREEQNTSYRVSVTILHODWLNGKEYKCKVSNKALPAPETISKAK 240

Qy 241 GQPREQVYTLPSRDELTKNQVSLTCLVKGFPSDIAVEWNSQOPENNYKTPPVLD 300  
Db 241 GQPREQVYTLPSRDELTKNQVSLTCLVKGFPSDIAVEWNSQOPENNYKTPPVLD 300

Qy 301 DGSEFFLKSQTLVTDKSRSQGNVFTCSVYHEALHNHYTQKSLSLSGK 347  
Db 301 DGSEFFLKSQTLVTDKSRSQGNVFTCSVYHEALHNHYTQKSLSLSGK 347

RESULT 3

US-08-459-657-43  
; Sequence 43, Application US/08459657  
; Patent No. 5914111  
; GENERAL INFORMATION:  
; APPLICANT: BIOGEN, INC.  
; APPLICANT: WALLNER, Barbara P.  
; APPLICANT: MILLER, Glenn T.  
; APPLICANT: ROSA, Margaret D.  
; TITLE OF INVENTION: CD2-B-BINDING DOMAIN OF LYMPHOCYTE  
; NUMBER OF SEQUENCES: 43  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Fish & Neave  
; STREET: 875 Third Avenue  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10022-6250  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/459,512  
; FILING DATE: 02-JUN-1995  
; CLASSIFICATION: 514  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US92/02050  
; FILING DATE: 12-MAR-1992  
; APPLICATION NUMBER: US 07/667,967  
; FILING DATE: 07-OCT-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: HALEY, James F., Jr.  
; REGISTRATION NUMBER: 27,794  
; REFERENCE/DOCKET NUMBER: B15C1P2  
; TELECOMMUNICATION INFORMATION:

APPLICATION NUMBER: PCT/US92/02050  
FILING DATE: 12-MAR-1992  
APPLICATION NUMBER: US 07/667,971  
FILING DATE: 12-MAR-1991

APPLICATION NUMBER: US/08/459,657  
FILING DATE: 02-JUN-1995  
CLASSIFICATION: 424  
PRIORITY APPLICATION DATA:  
APPLICANT NUMBER: PCT/US92/02050  
FILING DATE: 12-MAR-1992  
APPLICATION NUMBER: US 07/667,971  
FILING DATE: 12-MAR-1991

APPLICATION NUMBER: PCT/US92/02050  
FILING DATE: 12-MAR-1992  
APPLICATION NUMBER: US 07/667,971  
FILING DATE: 12-MAR-1991